

Sequence Comparison
us-09-876-790-1.rni

QY 484 GGGGTGACAGATAATTGAGACAGGAACACATTTGATTTTCATTTCAACCGATTGCG 543
Db 619 GGGGTGACAGATAATTGAGACAGGAACACATTTGATTTTCATTTCAACCGATTGCG 678
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 579
Db 679 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 714

RESULT 2

US-09-128-155-1
; Sequence 1, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (356)...(889)
US-09-128-155-1

Query Match 68.3%; Score 395.2; DB 3; Length 989;
Best Local Similarity 98.0%; Pred. No. 9.8e-122;
Matches 400; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATACGCCAGAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCG 231
Db 485 AATTGTTTCACACAAAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCG 544
QY 232 GAGAAAGGAAGTCCGATTCCTCTGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 291
Db 545 GAGAAAGGAAGTCCGATTCCTCTGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 604
QY 292 AAGGATAAAGGACAAAGTCAATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTG 351
Db 605 AAGGATAAAGGACAAAGTCAATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTG 664
QY 352 GCTGCCCAAAAGGAATCAGCAGCGCCGCTTCATCTTTATAGGGCTCAGGTGGCTCC 411
Db 665 GCTGCCCAAAAGGAATCAGCAGCGCCGCTTCATCTTTATAGGGCTCAGGTGGCTCC 724
QY 412 TGAACATGCTGAGTGGCGGCTCACCCTGGATGTCATCTGCACCTCTGCAATTGT 471
Db 725 TGAACATGCTGAGTGGCGGCTCACCCTGGATGTCATCTGCACCTCTGCAATTGT 784
QY 472 AATGAGCCTGTTGGGTGACAGATAAATTGAGAACAGGAACACATTTTCATT 531
Db 785 AATGAGCCTGTTGGGTGACAGATAAATTGAGAACAGGAACACATTTTCATT 844
QY 532 CAACCAAGTTGCAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 579
Db 845 CAACCAAGTTGCAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 892

RESULT 3
US-09-128-155-10
; Sequence 10, Application US/09128155
; Patent No. 6117654

; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-09-128-155-10

Query Match 67.7%; Score 392.2; DB 3; Length 408;
Best Local Similarity 98.0%; Pred. No. 6e-121;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATACGCCAGAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCG 231
Db 4 AATTGTTTCACACAAAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCG 63
QY 232 GAGAAAGGAAGTCCGATTCCTCTGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 291
Db 64 GAGAAAGGAAGTCCGATTCCTCTGGGGTCTCTAAAGGGAGTTTGTCTACTGTGAC 123
QY 292 AAGGATAAAGGACAAAGTCAATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTG 351
Db 124 AAGGATAAAGGACAAAGTCAATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTG 183
QY 352 GCTGCCCAAAAGGAATCAGCAGCGCCGCTTCATCTTTATAGGGCTCAGGTGGCTCC 411
Db 184 GCTGCCCAAAAGGAATCAGCAGCGCCGCTTCATCTTTATAGGGCTCAGGTGGCTCC 243
QY 412 TGAACATGCTGAGTGGCGGCTCACCCTGGATGTCATCTGCACCTCTGCAATTGT 471
Db 244 TGAACATGCTGAGTGGCGGCTCACCCTGGATGTCATCTGCACCTCTGCAATTGT 303
QY 472 AATGAGCCTGTTGGGTGACAGATAAATTGAGAACAGGAACACATTTTCATT 531
Db 304 AATGAGCCTGTTGGGTGACAGATAAATTGAGAACAGGAACACATTTTCATT 363
QY 532 CAACCAAGTTGCAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 576
Db 364 CAACCAAGTTGCAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 408

RESULT 4
US-09-128-155-6
; Sequence 6, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 3, 2003, 18:32:50 ; Search time 64 Seconds
(without alignments)
88.269 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRETETKGNKSFKKR.....IEFSFQPVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	895	88.0	218	4	US-09-293-625-2	Sequence 2, Appli
2	702	69.0	167	3	US-09-128-155-7	Sequence 7, Appli
3	702	69.0	178	3	US-09-128-155-2	Sequence 2, Appli
4	695	68.3	136	3	US-09-128-155-11	Sequence 11, Appli
5	623	61.3	115	3	US-09-128-155-5	Sequence 5, Appli
6	623	61.3	115	3	US-09-128-155-9	Sequence 9, Appli
7	623	61.3	115	3	US-09-128-155-13	Sequence 13, Appli
8	473.5	46.6	185	3	US-09-128-155-18	Sequence 18, Appli
9	225.5	22.2	169	2	US-08-790-032-2	Sequence 2, Appli
10	225.5	22.2	169	3	US-09-069-619-2	Sequence 2, Appli
11	225.5	22.2	169	4	US-09-494-018-2	Sequence 2, Appli
12	172.5	17.0	155	4	US-09-417-455-5	Sequence 5, Appli
13	172.5	17.0	155	4	US-09-348-942-5	Sequence 5, Appli
14	172.5	17.0	155	4	US-09-316-081-5	Sequence 5, Appli
15	172.5	17.0	155	4	US-09-578-458-5	Sequence 5, Appli
16	172.5	17.0	155	4	US-09-522-964A-5	Sequence 5, Appli
17	172.5	17.0	155	4	US-09-457-626-5	Sequence 5, Appli
18	165.5	16.3	152	4	US-09-578-458-18	Sequence 18, Appli
19	159	15.6	178	3	US-09-000-630C-21	Sequence 21, Appli
20	159	15.6	178	3	US-08-862-730C-21	Sequence 21, Appli
21	159	15.6	178	4	US-09-417-455-9	Sequence 9, Appli
22	159	15.6	178	4	US-09-348-942-9	Sequence 9, Appli
23	159	15.6	178	4	US-09-457-626-9	Sequence 9, Appli
24	155.5	15.3	152	4	US-09-316-081-2	Sequence 2, Appli
25	155.5	15.3	152	4	US-09-578-458-2	Sequence 2, Appli
26	155.5	15.3	152	4	US-09-522-964A-2	Sequence 2, Appli
27	155.5	15.3	153	3	US-08-677-778B-1	Sequence 1, Appli

28	155.5	15.3	169	4	US-09-316-081-4	Sequence 4, Appli
29	155.5	15.3	169	4	US-09-578-458-4	Sequence 4, Appli
30	155.5	15.3	169	4	US-09-522-964A-4	Sequence 4, Appli
31	155.5	15.3	200	4	US-09-578-458-13	Sequence 13, Appli
32	155.5	15.3	200	4	US-09-522-964A-13	Sequence 13, Appli
33	151.5	14.9	177	3	US-09-000-630C-22	Sequence 22, Appli
34	151.5	14.9	177	3	US-08-862-730C-22	Sequence 22, Appli
35	151.5	14.9	177	4	US-09-417-455-11	Sequence 11, Appli
36	151.5	14.9	177	4	US-09-348-942-11	Sequence 11, Appli
37	151.5	14.9	177	4	US-09-457-626-11	Sequence 11, Appli
38	150.5	14.8	180	1	US-08-476-860-13	Sequence 13, Appli
39	150.5	14.8	180	2	US-08-910-733-13	Sequence 13, Appli
40	150.5	14.8	180	2	US-08-910-884-13	Sequence 13, Appli
41	150.5	14.8	389	4	US-09-131-247-14	Sequence 14, Appli
42	149.5	14.7	153	3	US-08-798-414-2	Sequence 2, Appli
43	149.5	14.7	153	4	US-09-131-247-2	Sequence 2, Appli
44	149.5	14.7	153	4	US-09-131-247-4	Sequence 4, Appli
45	149.5	14.7	156	1	US-08-476-860-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293, 625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match 88.0%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.3e-98;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	24	PKYKLNLPKFFSIHDDHRYLVLDGSLIAVPDKNIRPEIFALASSLSASAEKGSPI	83
DB	50	PKYKLNLPKFFSIHDDHRYLVLDGSLIAVPDKNIRPEIFALASSLSASAEKGSPI	109
QY	84	LLGVSKGEFCLYCDKDKGQSHPSLQKKKLMKLAOKESARRPFIFRAYGVSWMMLES	143
DB	110	LLGVSKGEFCLYCDKDKGQSHPSLQKKKLMKLAOKESARRPFIFRAYGVSWMMLES	169
QY	144	AAHPGWFICTSCNCNEPVGYTDKFNKRIEFSFQPVCKAEMSPSEVSD	192
DB	170	AAHPGWFICTSCNCNEPVGYTDKFNKRIEFSFQPVCKAEMSPSEVSD	218

RESULT 2
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128, 155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091, 650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054, 646

Sequence Comparison B

see over

EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 7
LENGTH: 167
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-7

Sequence
Component
B

Query Match 69.0%; Score 702; DB 3; Length 167;
Best Local Similarity 93.6%; Pred. No. 2.3e-75;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0

OY 53 AVPDKNYIRPEIFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKE 112
DB 28 SLPTMNFVHTKIFFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKE 87
OY 113 KLMKLAQKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKH 172
DB 88 KLMKLAQKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKH 147
OY 173 IEFSPQVCKAEMSPSEVSD 192
DB 148 IEFSPQVCKAEMSPSEVSD 167

RESULT 3

US-09-128-155-2
Sequence 2, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 2
LENGTH: 178
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-2

Query Match 69.0%; Score 702; DB 3; Length 178;
Best Local Similarity 93.6%; Pred. No. 2.5e-75;
Matches 131; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

OY 53 AVPDKNYIRPEIFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKE 112
DB 39 SLPTMNFVHTKIFFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKE 98
OY 113 KLMKLAQKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKH 172
DB 99 KLMKLAQKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKH 158
OY 173 IEFSPQVCKAEMSPSEVSD 192
DB 159 IEFSPQVCKAEMSPSEVSD 178

RESULT 4

US-09-128-155-11
Sequence 11, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 11
LENGTH: 136
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-11

Query Match 68.3%; Score 695; DB 3; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.1e-74;
Matches 130; Conservative 3; Mismatches 2; Indels 0; Gaps 0

OY 58 NYRPEIFFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKEKLMKL 117
DB 2 NFVHTKIFFALASSLSASAEGSPILLGVSKGEFCLYCDKDGSHPSLQKKEKLMKL 61
OY 118 AAKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKHIEFSF 177
DB 62 AAKESARRPFIFYRAQVGSWMNLESAAHPGWFICTSCNCPVGVTDKFNKRKHIEFSF 121
OY 178 QPVCKAEMSPSEVSD 192
DB 122 QPVCKAEMSPSEVSD 136

RESULT 5

US-09-128-155-5
Sequence 5, Application US/09128155
Patent No. 6117654
GENERAL INFORMATION:
APPLICANT: Pan, Yang
TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 09404/052001
CURRENT APPLICATION NUMBER: US/09/128,155
CURRENT FILING DATE: 1998-08-03
EARLIER APPLICATION NUMBER: US 60/091,650
EARLIER FILING DATE: 1998-07-02
EARLIER APPLICATION NUMBER: US 60/054,646
EARLIER FILING DATE: 1997-08-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSeq for windows version 3.0
SEQ ID NO 5
LENGTH: 115
TYPE: PRT
ORGANISM: Homo sapiens
US-09-128-155-5

Query Match 61.3%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.1e-66;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 EKGSPILLGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGS 137
DB 1 EKGSPILLGVSKGEFCLYCDKDGSHPSLQKKEKLMKLAQKESARRPFIFYRAQVGS 60
OY 138 WNMLESAAHPGWFICTSCNCPVGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 192
DB 61 WNMLESAAHPGWFICTSCNCPVGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 115

RESULT 6

US-09-128-155-9
Sequence 9, Application US/09128155
Patent No. 6117654

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 3, 2003, 18:32:50 ; Search time 64 Seconds
(without alignments)
88.269 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRRETETKGNSEFKR.....IEFSQPVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	895	88.0	218	4	US-09-293-625-2 Sequence 2, Appli
2	702	69.0	167	3	US-09-128-155-7 Sequence 7, Appli
3	702	69.0	178	3	US-09-128-155-2 Sequence 2, Appli
4	695	68.3	136	3	US-09-128-155-11 Sequence 11, Appli
5	623	61.3	115	3	US-09-128-155-5 Sequence 5, Appli
6	623	61.3	115	3	US-09-128-155-9 Sequence 9, Appli
7	623	61.3	115	3	US-09-128-155-13 Sequence 13, Appli
8	473.5	46.6	185	3	US-09-128-155-18 Sequence 18, Appli
9	225.5	22.2	169	2	US-08-790-032-2 Sequence 2, Appli
10	225.5	22.2	169	3	US-09-069-619-2 Sequence 2, Appli
11	225.5	22.2	169	4	US-09-494-018-2 Sequence 2, Appli
12	172.5	17.0	155	4	US-09-417-455-5 Sequence 5, Appli
13	172.5	17.0	155	4	US-09-348-942-5 Sequence 5, Appli
14	172.5	17.0	155	4	US-09-316-081-5 Sequence 5, Appli
15	172.5	17.0	155	4	US-09-578-458-5 Sequence 5, Appli
16	172.5	17.0	155	4	US-09-522-964A-5 Sequence 5, Appli
17	172.5	17.0	152	4	US-09-578-458-18 Sequence 18, Appli
18	165.5	16.3	152	4	US-09-578-458-18 Sequence 18, Appli
19	159	15.6	178	3	US-09-000-630C-21 Sequence 21, Appli
20	159	15.6	178	3	US-08-862-730C-21 Sequence 21, Appli
21	159	15.6	178	4	US-09-417-455-9 Sequence 9, Appli
22	159	15.6	178	4	US-09-348-942-9 Sequence 9, Appli
23	159	15.6	178	4	US-09-457-626-9 Sequence 9, Appli
24	155.5	15.3	152	4	US-09-316-081-2 Sequence 2, Appli
25	155.5	15.3	152	4	US-09-578-458-2 Sequence 2, Appli
26	155.5	15.3	152	4	US-09-522-964A-2 Sequence 2, Appli
27	155.5	15.3	153	3	US-08-677-778B-1 Sequence 1, Appli

28	155.5	15.3	169	4	US-09-316-081-4	Sequence 4, Appli
29	155.5	15.3	169	4	US-09-578-458-4	Sequence 4, Appli
30	155.5	15.3	169	4	US-09-522-964A-4	Sequence 4, Appli
31	155.5	15.3	200	4	US-09-578-458-13	Sequence 13, Appli
32	155.5	15.3	200	4	US-09-522-964A-13	Sequence 13, Appli
33	151.5	14.9	177	3	US-09-000-630C-22	Sequence 22, Appli
34	151.5	14.9	177	3	US-08-862-730C-22	Sequence 22, Appli
35	151.5	14.9	177	4	US-09-417-455-11	Sequence 11, Appli
36	151.5	14.9	177	4	US-09-348-942-11	Sequence 11, Appli
37	151.5	14.9	177	4	US-09-457-626-11	Sequence 11, Appli
38	150.5	14.8	180	1	US-08-476-860-13	Sequence 13, Appli
39	150.5	14.8	180	2	US-08-910-733-13	Sequence 13, Appli
40	150.5	14.8	180	2	US-08-910-884-13	Sequence 13, Appli
41	150.5	14.8	389	4	US-09-131-247-14	Sequence 14, Appli
42	149.5	14.7	153	3	US-08-798-414-2	Sequence 2, Appli
43	149.5	14.7	153	4	US-09-131-247-2	Sequence 2, Appli
44	149.5	14.7	153	4	US-09-131-247-4	Sequence 4, Appli
45	149.5	14.7	156	1	US-08-476-860-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-09-293-625-2
; Sequence 2, Application US/09293625
; Patent No. 6342371
; GENERAL INFORMATION:
; APPLICANT: Young, Peter R.
; APPLICANT: McDonnell, Peter C
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
; FILE REFERENCE: GP-70607
; CURRENT APPLICATION NUMBER: US/09/293, 625
; CURRENT FILING DATE: 1999-04-16
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 2
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-293-625-2

Query Match 88.0%; Score 895; DB 4; Length 218;
Best Local Similarity 100.0%; Pred. No. 4.3e-98;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKLNPKKFSIHDDHKVLYLDSGNLIAVPDKNYIRPEIFALASSLSASAEKGSPI 83
Db 50 PKYKLNPKKFSIHDDHKVLYLDSGNLIAVPDKNYIRPEIFALASSLSASAEKGSPI 109
QY 84 LIGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 143
Db 110 LIGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 169
QY 144 AAHPGWFICTSCNENEPVGYTDKFEENRKHIEFSQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNENEPVGYTDKFEENRKHIEFSQPVCKAEMSPSEVSD 218

RESULT 2
US-09-128-155-7
; Sequence 7, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128, 155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091, 650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054, 646

```

; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
;
DS-09-128-155-7

```

Query Match	69.0%;	Score 702;	DB 3;	Length 167;
Best Local Similarity	93.6%;	Pred. No. 2.3e-75;		
Matches 131; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

QY	53	AVPDKNYIRPETIFEFALASSLSASAEKGPILLGVSKGEFCLYCDKDKGQSHPSLOJKE	112
	:::		
Db	28	SLPTMNFVHTKIFEFALASSLSASAEKGPILLGVSKGEFCLYCDKDKGQSHPSLOJKE	87
QY	113	KLMKLAQKESARRPETIFYRAQVGSNNMLESAAHPGMWICTSCNCPNPVGTDTKFEENKH	172
Db	88	KLMKLAQKESARRPETIFYRAQVGSNNMLESAAHPGMWICTSCNCPNPVGTDTKFEENKH	147
QY	173	IEFSFQPVCKAEMSPSEVSD	192
Db	148	IEFSFQPVCKAEMSPSEVSD	167

```

RESULT 3
US-09-128-155-2
; Sequence 2, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 178
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-2

```

	Query Match	69.0%;	Score 702;	DB 3;	Length 178;
	Best Local Similarity	93.6%;	Pred. No. 2.5e-75;		
	Matches 131;	Conservative	5;	Mismatches 4;	Indels 0; Gaps
QY	53 AVPDKNYIRPTEFFALASSLSASAEGKSPILLGVSKGEFCLCYCDKDKGQSHPSLQLKE	112			
Dd	39 SLPTMNFVHTKTFEFALASSLSASAEKGSPIILGVSKGEFCLCYCDKDKGQSHPSLQLKE	98			
QY	113 KLMLAAOKESARRPFIIFYRAQVGSNMULESAHPGMWICTSCNCNEPVGVTDTKFENRKH	172			
Dd	99 KLMLAAOKESARRPFIFYRAQVGSNMULESAHPGMWICTSCNCNEPVGVTDTKFENRKH	158			
QY	173 IEFSTQPYCKAEMSPSEVS D	192			
Dd	159 IEFSTQPYCKAEMSPSEVS D	178			

RESULT 4
US-09-128-155-11
; Sequence 11, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

```

; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-11

```

Query Match	68.3%;	Score 695;	DB 3;	Length 136;
Best Local Similarity	96.3%;	Pred. No. 1.1e-74;		
Matches 130; Conservative	3;	Mismatches 2;	Indels 0;	Gaps 0;

QY	58	NYIRPEIFEFALASSLSASAEKSGPILLVGSKGEFCLYCDKDGOSHPSLQLKKEKIMKL	117
		:: :	
Db	2	NEVHTKIFALASSLSASAEKSGPILLVGSKGEFCLYCDKDGQSHPSLQLKKEKIMKL	61
QY	118	AAQKESARRPFTFYRAQVGSWMNLESAAHPGWFICTSCNCNEBVGVTDKFENRKHIERSF	177
Db	62	AAQKESARRPFTFYRAQVGSWMNLESAAHPGWFICTSCNCNEBVGVTDKFENRKHIERSF	121
QY	178	QPVCKAEMSPSEVSD	192
Db	122	QPVCKAEMSPSEVSD	136

```

RESULT 5
US-09-128-155-5
; Sequence 5, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-128-155-5

```

	Query Match	61.3%;	Score 623;	DB 3;	Length 115;
	Best Local Similarity	100.0%;	Pred. No. 3.1e-66;		
	Matches 115;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	
QY	78	EKGSPIILGVSKGEFCLCYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIIFYRAQVGS	137		
Db	1	EKGSPIILGVSKGEFCLCYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIIFYRAQVGS	60		
QY	138	WNMLESAHPGKWFICTSCNCNENEPVGYTDKGFENRKHIIEFSFQPYCKAEMSPSEVSD	192		
Db	61	WNMLESAHPGKWFICTSCNCNENEPVGYTDKGFENRKHIIEFSFQPYCKAEMSPSEVSD	115		

RESULT 6
US-09-128-155-9
; Sequence 9, Application US/09128155
; Patent No. 6117654

```
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-128-155-9
```

```
Query Match          61.3%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.1e-66;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 78 EKGSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGS 137
      |||||||
Db 1 EKGSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGS 60
```

```
QY 138 WNMLESAAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 192
      |||||||
Db 61 WNMLESAAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 115
```

```
RESULT 7
US-09-128-155-13
; Sequence 13, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-128-155-13
```

```
Query Match          61.3%; Score 623; DB 3; Length 115;
Best Local Similarity 100.0%; Pred. No. 3.1e-66;
Matches 115; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 78 EKGSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGS 137
      |||||||
Db 1 EKGSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGS 60
```

```
QY 138 WNMLESAAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 192
      |||||||
Db 61 WNMLESAAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSFQPVCKAEMSPSEVSD 115
```

```
RESULT 8
US-09-128-155-18
; Sequence 18, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
```

```
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: synthetically generated
; LOCATION: (1)...(185)
; OTHER INFORMATION: human sequence predicted using an alignment algorithm which
; OTHER INFORMATION: predicts presence of alternatively spliced exons for a protei
; OTHER INFORMATION: interest in a stretch of genomic DNA
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(185)
; OTHER INFORMATION: Xaa = Any Amino Acid
; US-09-128-155-18
```

```
Query Match          46.6%; Score 473.5; DB 3; Length 185;
Best Local Similarity 91.8%; Pred. No. 3.3e-48;
Matches 90; Conservative 3; Mismatches 4; Indels 1; Gaps 1;
```

```
QY 68 LASSLSASAEEKSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRP 127
      |||||
Db 71 LSSLSASAEEKSPILLGVSKGEFLCYCDKDGQSHPSLQKKKLMKLAQKESARRP 129
```

```
QY 128 FIFYRAQGVSWNMLESAAHPGWFICTSCNCPNPGVTD 165
      |||||||
Db 130 FIFYRAQGVSWNMLESAAHPGWFICTSCNCPNPGVIXN 167
```

```
RESULT 9
US-08-790-032-2
; Sequence 2, Application US/08790032
; Patent No. 5863769
; GENERAL INFORMATION:
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Interleukin-1 Receptor Antagonist
; TITLE OF INVENTION: Beta (IL-1RA_)
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Smithkline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/790,032
; FILING DATE: 28-JAN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schreck, Patricia A
; REGISTRATION NUMBER: 33,777
; REFERENCE/DOCKET NUMBER: ATG50051
```

[illegible]

```

US-09-069-619-2

Query Match          22.2%; Score 225.5; DB 3; Length 169;
Best Local Similarity 38.3%; Pred. No. 7.6e-19;
Matches 51; Conservative 26; Mismatches 51; Indels 5; Gaps 4;

OY 35 SIHDQHKVLVDSCNLIAPDPKNYIRPEIFFALASSLSASAE-KGSPILGVSKGEFC 93
    :|:|:|:| | | | | | : : : | : | | | : | |
DB 26 TINDLNOQWTVLQGONLVAVPRSDSVTPVTVAVITCKYPEALEQGRDPIYLGIQNPEMC 85

OY 94 LYCDKDKGQSHPSLOLKKEKIMKLAQKESARRPFIFYRAQVGSWNMLESAAHPGFICT 153
    |||:| | | | | :|:|:|:| | | | :|:|:|:| | | | :|:| | | | |
DB 86 LYCEKVGEQ--PTQLKEQKIMDLYGQPEPV-KPFLFYRAKTGRTSTLESVAFPDWFIAS 142

OY 154 SCNCNEPVGVTDK 166
    | :|:|:| | :
DB 143 S-KRDQPILLTSE 154

RESULT 11
US-09-494-018-2
; Sequence 2, Application US/09494018
; Patent No. 6399573
; GENERAL INFORMATION:
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: INTERLEUKIN-1 RECEPTOR ANTAGONIST BETA
; FILE REFERENCE: ATG-50051-D1
; CURRENT APPLICATION NUMBER: US/09/494,018
; EARLIER FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 09/069,619
; EARLIER FILING DATE: 1998-04-29
; EARLIER APPLICATION NUMBER: 09/007,464
; EARLIER FILING DATE: 1998-01-14
; EARLIER APPLICATION NUMBER: 08/790,032
; EARLIER FILING DATE: 1997-01-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 169
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-494-018-2

Query Match          22.2%; Score 225.5; DB 4; Length 169;
Best Local Similarity 38.3%; Pred. No. 7.6e-19;
Matches 51; Conservative 26; Mismatches 51; Indels 5; Gaps 4;

OY 35 SIHDQHKVLVDSCNLIAPDPKNYIRPEIFFALASSLSASAE-KGSPILGVSKGEFC 93
    :|:|:|:| | | | | | : : : | : | | | : | |
DB 26 TINDLNOQWTVLQGONLVAVPRSDSVTPVTVAVITCKYPEALEQGRDPIYLGIQNPEMC 85

OY 94 LYCDKDKGQSHPSLOLKKEKIMKLAQKESARRPFIFYRAQVGSWNMLESAAHPGFICT 153
    |||:| | | | | :|:|:~::~|| | | | :|:|:|:| | | | :|:| | | | |
DB 86 LYCEKVGEQ--PTQLKEQKIMDLYGQPEPV-KPFLFYRAKTGRTSTLESVAFPDWFIAS 142

OY 154 SCNCNEPVGVTDK 166
    | :|:|:| | :
DB 143 S-KRDQPILLTSE 154

RESULT 12
US-09-417-455-5
; Sequence 5, Application US/09417455
; Patent No. 6294655
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Pace, Ann
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/36328
; CURRENT APPLICATION NUMBER: US/09/417,455
; CURRENT FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: US 09/348,942

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; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: PCT/US99/04291
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/287,210
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: US 09/251,370
; PRIOR FILING DATE: 1999-02-17
; PRIOR APPLICATION NUMBER: US 09/229,591
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 09/127,698
; PRIOR FILING DATE: 1998-07-31
; PRIOR APPLICATION NUMBER: US 09/099,818
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: US 09/082,364
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: US 09/079,909
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 09/055,010
; PRIOR FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-417-455-5
```

```
Query Match 17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHQDHKVLVLDGSLIAYPDKNYIRPEIFFALASSLSASAERG----- 80
| : | | | | : | | : | |
Db 9 FRMKDSALKVLYLHNQ-----LAGLHAGKVIKGEISVVPNRWLDA 52

QY 81 --SPILGVSKGEFCLYCDKDGQSHPSLQKKEKIMKL-AAQKESARRPFIYRAOVGS 137
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
Db 53 SLSPVILGVQGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107

QY 138 WNMLESAAHPGWFICTSCNCPNPGVTDKFEEN 169
: | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 108 TSSFESAAYPGWFLCTYPEADQPVRLTQLPEN 139
```

```
RESULT 13
US-09-348-942-5
; Sequence 5, Application US/09348942
; Patent No. 6337072
; GENERAL INFORMATION:
; APPLICANT: John Ford
; TITLE OF INVENTION: A NOVEL INTERLEUKIN-1 RECEPTOR ANTAGONIST AND USES THEREOF
; FILE REFERENCE: 28110/35801
; CURRENT FILING DATE: US/09/348,942
; EARLIER FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: PCT/US99/04291
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/287,210
; EARLIER FILING DATE: 1999-04-05
; EARLIER APPLICATION NUMBER: US 09/251,370
; EARLIER FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: US 09/229,591
; EARLIER FILING DATE: 1999-01-13
; EARLIER APPLICATION NUMBER: US 09/127,698
; EARLIER FILING DATE: 1998-07-31
; EARLIER APPLICATION NUMBER: US 09/099,818
; EARLIER FILING DATE: 1998-06-19
; EARLIER APPLICATION NUMBER: US 09/082,364
; EARLIER FILING DATE: 1998-05-20
; EARLIER APPLICATION NUMBER: US 09/079,909
; EARLIER FILING DATE: 1998-05-15
; EARLIER APPLICATION NUMBER: US 09/055,010
; EARLIER FILING DATE: 1998-04-03
; NUMBER OF SEQ ID NOS: 30
```

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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-348-942-5
```

```
Query Match 17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHQDHKVLVLDGSLIAYPDKNYIRPEIFFALASSLSASAERG----- 80
| : | | | | : | | : | |
Db 9 FRMKDSALKVLYLHNQ-----LAGLHAGKVIKGEISVVPNRWLDA 52

QY 81 --SPILGVSKGEFCLYCDKDGQSHPSLQKKEKIMKL-AAQKESARRPFIYRAOVGS 137
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
Db 53 SLSPVILGVQGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107

QY 138 WNMLESAAHPGWFICTSCNCPNPGVTDKFEEN 169
: | | | | | | | | : | : | : | : | : | : | : | : | : | : |
Db 108 TSSFESAAYPGWFLCTYPEADQPVRLTQLPEN 139
```

```
RESULT 14
US-09-316-081-5
; Sequence 5, Application US/09316081
; Patent No. 6339141
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/35659
; CURRENT FILING DATE: US/09/316,081
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-316-081-5
```

```
Query Match 17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;
```

```
QY 34 FSIHQDHKVLVLDGSLIAYPDKNYIRPEIFFALASSLSASAERG----- 80
| : | | | | : | | : | |
Db 9 FRMKDSALKVLYLHNQ-----LAGLHAGKVIKGEISVVPNRWLDA 52

QY 81 --SPILGVSKGEFCLYCDKDGQSHPSLQKKEKIMKL-AAQKESARRPFIYRAOVGS 137
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
Db 53 SLSPVILGVQGSQCLSC--GVGQ-EPTLTLEPVNIMELYLGAKES--KSFTFYRRDMGL 107

QY 138 WNMLESAAHPGWFICTSCNCPNPGVTDKFEEN 169
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Db 108 TSSFESAAYPGWFLCTYPEADQPVRLTQLPEN 139
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RESULT 15
US-09-578-458-5
; Sequence 5, Application US/09578458
; Patent No. 6365726
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
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; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; PRIOR FILING DATE: 1999-03-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-578-458-5

Query Match 17.0%; Score 172.5; DB 4; length 155;
Best Local Similarity 33.6%; Pred. No. 1.3e-12;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;

QY 34 FSIHQDQHKVVLVLDGSLIAVPDKNYIRPEIFFALASSISASAEGK----- 80
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Db 9 FRMKDSALKVLYLHNNQL-----LAGGLHAGKVITKGEEISVVPNRWLDA 52

QY 81 --SPILGVSKGEFCLYCDKDKGSHPSLQKKKIMKL-AAOKESARRPFIYRAOVGS 137
| : | | | | | | | | | : | | : | | : | | : | |
Db 53 SLSPVILGVQGGSQLSC--GVGQ-EPTLTLEPVNIMELYLIGAKES--KSFTFYRDMGL 107

QY 138 WNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 169
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Db 108 TSSFEASAIPGWFLCTVPEADQPVRLTQLPEN 139

Search completed: May 3, 2003, 18:40:10
Job time : 67 secs

GenCore version 5.1.4_p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 05:23:36 ; Search time 99 Seconds
(without alignments)
1793.594 Million cell updates/sec

Title: US-09-876-790-1
Perfect score: 579
Sequence: 1 atgtcagcgtgtgatagag.....ccagtgcagcagcatag 579

Scoring table: IDENTIFY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA:*
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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	512.8	88.6	802	4	US-09-293-625-1 Sequence 1, Appl
2	395.2	68.3	989	3	US-09-128-155-1 Sequence 1, Appl
3	392.2	67.7	408	3	US-09-128-155-10 Sequence 10, Appl
4	392.2	67.7	501	3	US-09-128-155-6 Sequence 6, Appl
5	392.2	67.7	534	3	US-09-128-155-3 Sequence 3, Appl
6	251	43.4	176373	3	US-09-128-155-17 Sequence 17, Appl
7	51.2	8.8	1183	2	US-08-790-032-1 Sequence 1, Appl
8	51.2	8.8	1183	3	US-09-069-619-1 Sequence 1, Appl
9	51.2	8.8	1183	4	US-09-494-018-1 Sequence 1, Appl
10	37.2	6.4	7218	1	US-08-232-463-14 Sequence 14, Appl
11	36.6	6.3	537	3	US-09-000-630C-25 Sequence 25, Appl
12	36.6	6.3	537	3	US-08-862-730C-25 Sequence 25, Appl
13	36.6	6.3	6350	4	US-09-647-826-1 Sequence 1, Appl
14	35.6	6.1	2983	3	US-09-058-489-86 Sequence 86, Appl
15	35.6	6.1	4388	4	US-09-578-458-16 Sequence 16, Appl
16	35.6	6.1	9439	3	US-09-058-489-89 Sequence 89, Appl
17	34.8	6.0	357	4	US-09-417-455-1 Sequence 1, Appl
18	34.8	6.0	357	4	US-09-348-942-1 Sequence 1, Appl
19	34.8	6.0	357	4	US-09-457-626-1 Sequence 1, Appl
20	34.8	6.0	462	3	US-08-798-414-1 Sequence 1, Appl
21	34.8	6.0	462	4	US-09-131-247-1 Sequence 1, Appl
22	34.8	6.0	474	1	US-08-476-860-9 Sequence 9, Appl
23	34.8	6.0	474	2	US-08-910-733-9 Sequence 9, Appl
24	34.8	6.0	474	2	US-08-910-884-9 Sequence 9, Appl
25	34.8	6.0	514	1	US-08-284-784-41 Sequence 41, Appl
26	34.8	6.0	514	2	US-08-854-811-41 Sequence 41, Appl
27	34.8	6.0	531	2	US-08-809-185-1 Sequence 1, Appl

28	34.8	6.0	534	3	US-09-000-630C-24	Sequence 24, Appl
29	34.8	6.0	534	3	US-08-862-730C-24	Sequence 24, Appl
30	34.8	6.0	543	1	US-08-422-655-1	Sequence 1, Appl
31	34.8	6.0	579	1	US-08-476-860-12	Sequence 12, Appl
32	34.8	6.0	579	2	US-08-910-733-12	Sequence 12, Appl
33	34.8	6.0	579	2	US-08-910-884-12	Sequence 12, Appl
34	34.8	6.0	602	1	US-08-459-811-1	Sequence 1, Appl
35	34.8	6.0	602	1	US-08-459-092-1	Sequence 1, Appl
36	34.8	6.0	602	2	US-08-459-814-1	Sequence 1, Appl
37	34.8	6.0	602	2	US-08-425-232-1	Sequence 1, Appl
38	34.8	6.0	602	2	US-08-471-227-2	Sequence 2, Appl
39	34.8	6.0	603	1	US-08-484-598-1	Sequence 1, Appl
40	34.8	6.0	603	2	US-08-479-140-1	Sequence 1, Appl
41	34.8	6.0	603	3	US-08-477-143-1	Sequence 1, Appl
42	34.8	6.0	717	1	US-08-284-784-40	Sequence 40, Appl
43	34.8	6.0	717	2	US-08-854-811-40	Sequence 40, Appl
44	34.8	6.0	985	4	US-09-417-455-2	Sequence 2, Appl
45	34.8	6.0	985	4	US-09-348-942-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-293-625-1
Sequence 1, Application US/09293625
Patent No. 6342371
GENERAL INFORMATION:
APPLICANT: Young, Peter R.
APPLICANT: McDonnell, Peter C
TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOGUE, IL-1H4
FILE REFERENCE: GP-70607
CURRENT APPLICATION NUMBER: US/09/293, 625
CURRENT FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 802
TYPE: DNA
ORGANISM: Homo sapiens
US-09-293-625-1

QY	64	AGAGTCCAAAGGTGAAGACTTAACCCGAAGAAATTCAGCATTCATGACGAGATCAC	123
DB	199	ACAAGTCCAAAGGTGAAGACTTAACCCGAAGAAATTCAGCATTCATGACGAGATCAC	258
QY	124	AAAGTACTGCTCTGACTCTGGCAATCTCATAGCAGTCCAGATAAAACTACATACGC	183
DB	259	AAAGTACTGCTCTGACTCTGGCAATCTCATAGCAGTCCAGATAAAACTACATACGC	318
QY	184	CCAGAGATCTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTCGGAGAAAGAGT	243
DB	319	CCAGAGATCTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTCGGAGAAAGAGT	378
QY	244	CCGATTCCTCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGA	303
DB	379	CCGATTCCTCGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGA	438
QY	304	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	363
DB	439	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	498
QY	364	GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	423
DB	499	GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	558
QY	424	GAGTCGGCGGCTTACCCCGGATGTTTCATCTGCACCTCTGCAATTGATGAGCTGTT	483
DB	559	GAGTCGGCGGCTTACCCCGGATGTTTCATCTGCACCTCTGCAATTGATGAGCTGTT	618

QY 484 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCATTTCAACCGATTGCG 543
Db 619 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCATTTCAACCGATTGCG 678
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 579
Db 679 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 714

RESULT 2

US-09-128-155-1
; Sequence 1, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (356)...(889)
US-09-128-155-1

Query Match 68.3%; Score 395.2; DB 3; Length 989;
Best Local Similarity 98.0%; Pred. No. 9.8e-122;
Matches 400; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATAGCCGAGAGATCTTCTTTGATTTAGCCTTCATCTTGAGCTCAGCCTCTGCG 231
Db 485 AATTTTGTTCACACAAGATCTTCTTTGATTTAGCCTTCATCTTGAGCTCAGCCTCTGCG 544
QY 232 GAGAAAGGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTTACTGTGAC 291
Db 545 GAGAAAGGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTTACTGTGAC 604
QY 292 AAGGATAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTG 351
Db 605 AAGGATAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTG 664
QY 352 GCTGCCCCAAAAGGATCAGCAGCGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC 411
Db 665 GCTGCCCCAAAAGGATCAGCAGCGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC 724
QY 412 TGGACATGCTGAGTGGCGGCTCAGCCCGGATGTTTCATCTGCACTCCTGCAATTGT 471
Db 725 TGGACATGCTGAGTGGCGGCTCAGCCCGGATGTTTCATCTGCACTCCTGCAATTGT 784
QY 472 AATGAGCCTGTGGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCATTT 531
Db 785 AATGAGCCTGTGGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCATTT 844
QY 532 CAACCAAGTTTGAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 579
Db 845 CAACCAAGTTTGAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 892

RESULT 3
US-09-128-155-10
; Sequence 10, Application US/09128155
; Patent No. 6117654

GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 408
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(408)
US-09-128-155-10

Query Match 67.7%; Score 392.2; DB 3; Length 408;
Best Local Similarity 98.0%; Pred. No. 6e-121;
Matches 397; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 172 AACTACATAGCCGAGAGATCTTCTTTGATTTAGCCTTCATCTTGAGCTCAGCCTCTGCG 231
Db 4 AATTTTGTTCACACAAGATCTTCTTTGATTTAGCCTTCATCTTGAGCTCAGCCTCTGCG 63
QY 232 GAGAAAGGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTTACTGTGAC 291
Db 64 GAGAAAGGAAGTCCGATTTCTCTGGGGGCTCTAAAGGGAGTTTGTCTTACTGTGAC 123
QY 292 AAGGATAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTG 351
Db 124 AAGGATAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTG 183
QY 352 GCTGCCCCAAAAGGATCAGCAGCGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC 411
Db 184 GCTGCCCCAAAAGGATCAGCAGCGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC 243
QY 412 TGGACATGCTGAGTGGCGGCTCAGCCCGGATGTTTCATCTGCACTCCTGCAATTGT 471
Db 244 TGGACATGCTGAGTGGCGGCTCAGCCCGGATGTTTCATCTGCACTCCTGCAATTGT 303
QY 472 AATGAGCCTGTGGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCATTT 531
Db 304 AATGAGCCTGTGGGGTGACAGATAATTGAGAACAGAAACATTTGATTTTCATTT 363
QY 532 CAACCAAGTTTGAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 576
Db 364 CAACCAAGTTTGAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 408

RESULT 4
US-09-128-155-6
; Sequence 6, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; EARLIER FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6

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; ; LENGTH: 501
; ; TYPE: DNA
; ; ORGANISM: Homo sapiens
; ; FEATURE:
; ; NAME/KEY: CDS
; ; LOCATION: (1)...(501)
; ; US-09-128-155-6

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Query Match	67.7%;	Score 392.2;	DB 3;	Length 501;
Best Local Similarity	98.0%;	Pred. No. 6.7e-121;		
Matches 397; Conservative	0;	Mismatches 8;	Indels 0;	Gaps 0;

QY	172	AAC	TAC	TAC	ACG	CC	CC	CAG	AG	AT	CT	TT	TG	CA	TT	AG	CC	TCA	TC	CT	TG	AG	CT	CAG	CC	CT	CG	231			
Db	97	AAT	TTT	GT	TT	CA	CA	CA	AA	GA	CT	TT	TG	CA	TT	AG	CC	TCA	TC	CT	TG	AG	CT	CAG	CC	CT	CG	156			
QY	232	GAG	AA	AG	GAG	AG	TCC	GAT	TT	CT	CT	GG	GG	GT	CT	TA	AA	GG	GG	AG	TT	TG	CT	CT	AG	CT	GC	291			
Db	157	GAG	AA	AG	GAG	AG	TCC	GAT	TT	CT	CT	GG	GG	GT	CT	TA	AA	GG	GG	AG	TT	TG	CT	CT	AG	CT	GC	216			
QY	292	AAG	AT	TA	AA	AG	GAC	AA	AG	TCA	TC	CC	TT	CAG	CT	GA	AG	AG	GAG	AA	ACT	GAT	GA	AG	CT	G	351				
Db	217	AAG	AT	TA	AA	AG	GAC	AA	AG	TCA	TC	CC	TT	CAG	CT	GA	AG	AG	GAG	AA	ACT	GAT	GA	AG	CT	G	276				
QY	352	GCT	G	CC	CA	AA	AA	GGA	AT	CAG	CAC	GC	GC	GC	CT	TCA	T	CT	T	T	A	T	AG	GC	T	CAG	T	GC	411		
Db	277	GCT	G	CC	CA	AA	AA	GGA	AT	CAG	CAC	GC	GC	GC	CT	TCA	T	CT	T	T	A	T	AG	GC	T	CAG	T	GC	336		
QY	412	TG	GA	CA	TG	CT	GG	AG	TG	CG	CG	GT	CA	CC	CC	GG	AT	GG	T	CA	T	GC	AC	CT	CT	GC	AA	T	GT	471	
Db	337	TG	GA	CA	TG	CT	GG	AG	TG	CG	CG	GT	CA	CC	CC	GG	AT	GG	T	CA	T	GC	AC	CT	CT	GC	AA	T	GT	396	
QY	472	AAT	G	AG	CC	TG	TT	GG	GG	TG	AC	AG	AT	TA	TT	TG	AG	AC	AG	GA	AA	CA	CA	T	TG	AA	TT	TT	CA	TT	531
Db	397	AAT	G	AG	CC	TG	TT	GG	GG	TG	AC	AG	AT	TA	TT	TG	AG	AC	AG	GA	AA	CA	CA	T	TG	AA	TT	TT	CA	TT	456
QY	532	CA	AC	CA	GT	TT	GC	AA	AG	CT	GA	AA	TG	AG	CC	CC	AG	TG	AG	GT	CA	GC	GA	T	576						
Db	457	CA	AC	CA	GT	TT	GC	AA	AG	CT	GA	AA	TG	AG	CC	CC	AG	TG	AG	GT	CA	GC	GA	T	501						

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RESULT 5
US-09-128-155-3
; Sequence 3, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for windows Version 3.0
; SEQ ID NO 3
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-128-155-3

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[illegible]

Db	190	GAGAAAGGAGCTCCGATTCTCCTGGGGCTCTTAAGGGAGCTTTGTCTCTACTGTGAC	249
QY	292	AAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTG	351
Db	250	AAGGATAAAGACAAAGTCATCCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTG	309
QY	352	GCTGCCCAAAGGAATCAGCACGCGGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC	411
Db	310	GCTGCCCAAAGGAATCAGCACGCGGCCCTTCATCTTTATAGGCTCAGGTGGGCTCC	369
QY	412	TGGAACATGCTTGAGAGTCGGCGGCTCACCCCGGATGGTTTCATCTGCACCTCCTGCAATTGT	471
Db	370	TGGAACATGCTTGAGAGTCGGCGGCTCACCCCGGATGGTTTCATCTGCACCTCCTGCAATTGT	429
QY	472	AATGAGCCTGTTGGGGTGACAGATAAATTGAGAACAGGAAACACATTGAAATTTTCATT	531
Db	430	AATGAGCCTGTTGGGGTGACAGATAAATTGAGAACAGGAAACACATTGAAATTTTCATT	489
QY	532	CAACCAAGTTTGCAAAAGCTGAATGAGCCCCAGTGAGGTCAGCGAT	576
Db	490	CAACCAAGTTTGCAAAAGCTGAATGAGCCCCAGTGAGGTCAGCGAT	534

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RESULT 6
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

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Query Match	43.4%;	Score 251;	DB 3;	Length 176373;
Best Local Similarity	100.0%;	Pred. No. 1.8e-72;		
Matches 251;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY 329 AGAAGGAGAACTGATGAAGCTGGCTGCCCAAAGGAATCAGCACGCGCCCTTCATCT				388
Db 158957 AGAAGGAGAACTGATGAAGCTGGCTGCCCAAAGGAATCAGCACGCGCCCTTCATCT				159016
QY 389 TTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGATGCT				448
Db 159017 TTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTGGAGTCGGCGGCTCACCCCGGATGCT				159076
QY 449 TCATCTGCACCTCCTGCAATTGTATGAGCCTGTTGGGCTGACAGATAAATTTGAGAACA				508
Db 159077 TCATCTGCACCTCCTGCAATTGTATGAGCCTGTTGGGCTGACAGATAAATTTGAGAACA				159136
QY 509 GGAACACATTTGAATTTTCATTTTCAACCCAGTTTGCACCAAGCTGAATGAGCCCCAGTGAGG				568
Db 159137 GGAACACATTTGAATTTTTCATTTTCAACCCAGTTTGCACCAAGCTGAATGAGCCCCAGTGAGG				159196
QY 569 TCAGCGATTAG 579				


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Query Match          6.3%; Score 36.6; DB 4; Length 6350;
Best Local Similarity 53.1%; Pred. No. 0.076;
Matches 78; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 357 CCAAAAGGAATCAGACGCGGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTGGAA 416
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4358 CAAGACAAAGAAGAGACAGACGCGCTTACCTTCATCCGCTCTGAGAAAGGCCACCAC 4417

QY 417 CATGCTGGAGTCGGCGGCTCACCCCGGATGTTCACTGCACTCCTCGCAATTGTAATGA 476
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4418 CAGCTTTGAGTCAGCTGCCCTGTCCAGGATGTTCTCTGCAACACACTAGAGGCTGACCG 4477

QY 477 GCCTGTGGGTGACAGATTAATTGTA 503
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 4478 TCCTGTGAGCCTCACCAACACACCGGA 4504

RESULT 14
US-09-058-489-86
; Sequence 86, Application US/09058489
; Patent No. 6103886
; GENERAL INFORMATION:
; APPLICANT: Whitehead Institute for Biomedical Research
; APPLICANT: Lahn, Bruce
; APPLICANT: Page, David
; TITLE OF INVENTION: Genes in the No. 6103886-Recombining Region of
; TITLE OF INVENTION: the Y Chromosome
; FILE REFERENCE: WH197-08PA
; CURRENT APPLICATION NUMBER: US/09/058,489
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/041,877
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 86
; LENGTH: 2983
; TYPE: DNA
; ORGANISM: Human
US-09-058-489-86

Query Match          6.1%; Score 35.6; DB 3; Length 2983;
Best Local Similarity 45.8%; Pred. No. 0.11;
Matches 119; Conservative 1; Mismatches 140; Indels 0; Gaps 0;

QY 2 TGTGAGGCTGTGATAGGAGGGAACAGAAACCAAGAAAGAACAGCTTTAAGACGCT 61
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Db 1156 TGACAGCCGGGAAAGAAATTTATTGACGACAGAAAGAACCAACCTTTTGACAAGCGGT 1215

QY 62 TAAGAGTCCAAAGTGAGAACTTAACCCGAGAAATTCAGCATTCATGACCAGGATC 121
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Db 1216 TGGCTTTCAGTGTGAGGACAGACAGAGAGTGCTTACAGATACAGAGATATTGCTCAGGA 1275

QY 122 ACAAGTACTGTCCTGGACTCTGGGAATCTCATAGCAGTTCCAGATAAAACTACATAC 181
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Db 1276 AGCAAGATGGCTTCAACCCACATCTTGTATTCACAAAATCGTCAGAGATTAACCTCACTAA 1335

QY 182 GCCCAGAGATCTTCTTTGCAATTAGCCTCATCTTGAGCTCAGCCTCTGCGGAGAAAGGAA 241
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QY 242 GTCCGATTCTCTGGGGGTC 261
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Db 1396 AGCTGTTCTGCTCAGCGCC 1415

RESULT 15
US-09-578-458-16
; Sequence 16, Application US/09578458
; Patent No. 6365726
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis G.
; APPLICANT: Ford, John
; APPLICANT: Ho, Alice
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; APPLICANT: Lin, Hai Shan
; APPLICANT: Pace, Ann M.
; TITLE OF INVENTION: Interleukin-1 Hy2 Materials and Methods
; FILE REFERENCE: 28110/36479
; CURRENT APPLICATION NUMBER: US/09/578,458
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/522,964
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 09/316,086
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 4388
; TYPE: DNA
; ORGANISM: Mouse
US-09-578-458-16
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Best Local Similarity 50.0%; Pred. No. 0.13;
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QY 382 TTCATCTTTATAGGGCTCAGGTGGCTCCTGGAACATGCTGGAGTGGCGGCTCACCCC 441
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QY 442 GGATGTTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTGGGTGACAGATAAATT 501
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QY 502 GAGACAGAAACACATTTGAATTTTCAATTTCAACCAAGTTTGCAAAAGCTGAAATGAGCC 559
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Search completed: May 3, 2003, 06:31:32
Job time : 203 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 04:04:12 ; Search time 1797 Seconds

(without alignments)
9377.031 Million cell updates/sec

Title: US-09-876-790-1

Perfect score: 579

Sequence: 1 atgtcagcgtgtgatatagag.....ccagtgcagtcacgcatag 579

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	517.8	89.4	594	9 AY071840	AY071840 Homo sapi
3	512.8	88.6	657	9 AF251119	AF251119 Homo sapi
4	512.8	88.6	760	9 BC020637	BC020637 Homo sapi
5	512.8	88.6	787	9 AF167368	AF167368 Homo sapi
6	512.8	88.6	793	9 AF200496	AF200496 Homo sapi
7	512.8	88.6	802	6 AR183757	AR183757 Sequence
8	512.8	88.6	817	9 AF251118	AF251118 Homo sapi
9	512.8	88.6	847	6 AX133934	AX133934 Sequence
10	512.8	88.6	855	6 AX133936	AX133936 Sequence
11	509.6	88.0	630	6 AX048211	AX048211 Sequence
12	504	87.0	754	6 AX092410	AX092410 Sequence
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15	310.8	53.7	575	6 AX133932	AX133932 Sequence
16	251	43.4	154214	9 AC079753	AC079753 Homo sapi
17	178	30.7	248	6 AX133933	AX133933 Sequence
18	113.2	19.6	118	6 AX133931	AX133931 Sequence
19	68.8	11.9	187395	2 AC096974	AC096974 Rattus no
20	57.6	9.9	187395	2 AC096974	AC096974 Rattus no
21	51.2	8.8	648	10 AY071842	AY071842 Mus muscu
22	51.2	8.8	1073	6 AX207820	AX207820 Sequence
23	51.2	8.8	1177	9 AF206696	AF206696 Homo sapi
24	51.2	8.8	1183	6 AR212173	AR212173 Sequence
25	51.2	8.8	1183	6 E54910	E54910 Interleukin
26	51.2	8.8	1183	9 AF200492	AF200492 Homo sapi
27	48.6	8.4	520	6 AX193587	AX193587 Sequence
28	48.6	8.4	585	6 AX052581	AX052581 Sequence
29	48.6	8.4	585	9 AF201833	AF201833 Homo sapi
30	48.6	8.4	1244	6 AX167128	AX167128 Sequence
31	47.6	8.2	329	6 AX193643	AX193643 Sequence
32	47.6	8.2	477	9 AF201831	AF201831 Homo sapi
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34	43.8	7.6	1321	6 AX491202	AX491202 Sequence
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36	41.4	7.2	36879	2 CEK07H11	Z81566 Caenorhabdt
37	40.6	7.0	465	6 AX080399	AX080399 Sequence
38	40.6	7.0	468	6 AX069335	AX069335 Sequence
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40	40.6	7.0	1283	10 AF200495	AF200495 Mus muscu
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ALIGNMENTS

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LOCUS AF201832 579 bp mRNA linear PRI 16-JAN-2000
DEFINITION Homo sapiens FIIL1 zeta mRNA, complete cds.
ACCESSION AF201832
VERSION AF201832.1 GI:6694391
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SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiindae; Homo.
REFERENCE
1 (bases 1 to 579)
Smith,D.E., Renshaw,B.R., Ketchem,R.R., Kubin,M., Garka,K.E. and
Sims,J.E.
TITLE
Four new members expand the interleukin-1 superfamily

JOURNAL J. Biol. Chem. 275 (2), 1169-1175 (2000)
MEDLINE 20092888
PUBMED 10625660
REFERENCE 2 (bases 1 to 579)
AUTHORS Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (04-NOV-1999) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
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Best Local Similarity 100.0%; Pred. No. 9.8e-169;
Matches 579; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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AY071840
LOCUS AY071840 594 bp mRNA linear PRI 20-MAY-2002
DEFINITION Homo sapiens IL-1F7d (IL1F7) mRNA, complete cds, alternatively
spliced.
ACCESSION AY071840
VERSION AY071840.1 GI:19068183
KEYWORDS
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Taylor,S.L., Renshaw,B.R., Garka,K.E., Smith,D.E. and Sims,J.E.
TITLE 1 (bases 1 to 594)
JOURNAL Taylor,S.L., Renshaw,B.R., Garka,K.E., Smith,D.E. and Sims,J.E.
MEDLINE Genomic organization of the interleukin-1 locus
PUBMED 21988051
11991723
REFERENCE 2 (bases 1 to 594)
AUTHORS Taylor,S.L., Renshaw,B.R., Garka,K.E., Smith,D.E. and Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Molecular Genetics, Immunex Corporation, 51 University Street, Seattle, WA 98101, USA
FEATURES
source location/Qualifiers
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QY 119 ATCACAAGTACTGCTGCTGAGCTGGAATCTCATAGCAGTCCAGATTAATACTACA 178
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Db 554 TTGCAAAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 594
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DEFINITION complete cds; alternatively spliced.
ACCESSION AF251119
VERSION AF251119.1 GI:10185737
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 657)
AUTHORS Pan,G., Risser,P., Mao,W., Baldwin,D.T., Zhong,A.W., Filvaroff,E.,
Yansura,D., Lewis,L., Eigenbrot,C., Henzel,W.J. and Vandlen,R.
TITLE IL-1H, an interleukin 1-related protein that binds IL-18
JOURNAL receptor/IL-1Rrp
MEDLINE Cytokine 13 (1), 1-7 (2001)
21066552
PUBMED 11145836
REFERENCE 2 (bases 1 to 657)
AUTHORS Pan,G., Baldwin,D.T. and Zhong,A.W.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way,
South San Francisco, CA 94080, USA
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Best Local Similarity 99.6%; Pred. No. 3.9e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 622 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 657
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BC020637 760 bp mRNA linear PRI 08-JAN-2002
LOCUS Homo sapiens, clone MGC:22276 IMAGE:4731213, mRNA, complete cds.
DEFINITION BC020637
ACCESSION BC020637
VERSION BC020637.1 GI:18088327
KEYWORDS MGC.
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 760)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE Strausberg,R.
JOURNAL Direct Submission
Submitted (03-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcdéparil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.
FEATURES
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JOURNAL Submitted (01-NOV-1999) Bone and Cartilage Biology, UW 2109,
Smithkline Beecham Pharmaceuticals, 709 Swedeland Rd., King of
Prussia, PA 19406, USA
FEATURES Location/Qualifiers

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BASE COUNT 241 a 188 c 182 g 182 t

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Best Local Similarity 99.6%; Pred. No. 4e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGACTTAAACCCGAGAATTCAGCATTCATGACCAGATCAC 123

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QY 124 AAAGTACTGTCTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC 183

Db 250 AAAGTACTGTCTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC 309

QY 184 CCAGAGATCTTCTTGGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGAGAAAGGAAGT 243

Db 310 CCAGAGATCTTCTTGGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGAGAAAGGAAGT 369

QY 244 CCGATTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAGGA 303

Db 370 CCGATTCTCTGGGGGTCTTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAGGA 429

QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAAGGAAACTGATGAAGCTGGCTGCCCAAAAG 363

Db 430 CAAAGTCATCCATCCCTTCAGCTGAAGAAGGAAACTGATGAAGCTGGCTGCCCAAAAG 489

QY 364 GAATCAGACGCGCGCCTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423

Db 490 GAATCAGACGCGCGCCTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 549

QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTTCAATTTGAATGAGCCTGTT 483

Db 550 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTTCAATTTGAATGAGCCTGTT 609

QY 484 GGGGTGACAGATAAATTGAGAACAGGAAACACATTTGCAATTTCAACACAGTTTGC 543

Db 610 GGGGTGACAGATAAATTGAGAACAGGAAACACATTTGCAATTTCAACACAGTTTGC 669

QY 544 AAAGCTGAATGAGCCCCCAGTGAGCTCAGCGATTAG 579

Db 670 AAAGCTGAATGAGCCCCCAGTGAGCTCAGCGATTAG 705

RESULT 7 ARI83757 802 bp DNA linear PAT 20-APR-2002

LOCUS ARI83757

DEFINITION Sequence 1 from patent us 6342371.

ACCESSION ARI83757

VERSION ARI83757.1 GI:20227726

KEYWORDS

SOURCE Unknown.

ORGANISM

Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 802)

AUTHORS McDonnell,P.C. and Young,P.R.

JOURNAL Interleukin-1 homologue, IL-1H4

Patent: US 6342371-A 1 29-JAN-2002;

FEATURES Location/Qualifiers

source

1..802

/organism="unknown"

BASE COUNT 243 a 190 c 185 g 184 t

ORIGIN

Query Match 88.6%; Score 512.8; DB 6; Length 802;
Best Local Similarity 99.6%; Pred. No. 4e-148;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGACTTAAACCCGAGAATTCAGCATTCATGACCAGATCAC 123

Db 199 ACAAGTCCAAAGGTGAAGACTTAAACCCGAGAATTCAGCATTCATGACCAGATCAC 258

QY 124 AAAGTACTGTCTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC 183

Db 259 AAAGTACTGTCTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC 318

QY 184 CCAGAGATCTTCTTGGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGAGAAAGGAAGT 243

Db 319 CCAGAGATCTTCTTGGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGAGAAAGGAAGT 378

QY 244 CCGATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAGGA 303

Db 379 CCGATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAGGA 438

QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAAGGAAACTGATGAAGCTGGCTGCCCAAAAG 363

Db 439 CAAAGTCATCCATCCCTTCAGCTGAAGAAGGAAACTGATGAAGCTGGCTGCCCAAAAG 498

QY 364 GAATCAGACGCGCGCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423

Db 499 GAATCAGACGCGCGCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 558

QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTTCAATTTGAATGAGCCTGTT 483

Db 559 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTTCAATTTGAATGAGCCTGTT 618

QY 484 GGGGTGACAGATAAATTGAGAACAGGAAACACATTTGCAATTTCAACACAGTTTGC 543

Db 619 GGGGTGACAGATAAATTGAGAACAGGAAACACATTTGCAATTTCAACACAGTTTGC 678

QY 544 AAAGCTGAATGAGCCCCCAGTGAGCTCAGCGATTAG 579

Db 679 AAAGCTGAATGAGCCCCCAGTGAGCTCAGCGATTAG 714

RESULT 8 AF251118 817 bp mRNA linear PRI 03-MAY-2001

LOCUS AF251118

DEFINITION Homo sapiens interleukin-1-related protein long isoform a mRNA,

complete cds; alternatively spliced.

ACCESSION AF251118

VERSION AF251118.1 GI:10185735

KEYWORDS

SOURCE

ORGANISM

Homo sapiens.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 817)

AUTHORS Pan,G., Risser,P., Mao,W., Baldwin,D.T., Zhong,A.W., Filvaroff,E.,

Yansura,D., Lewis,L., Eigenbrot,C., Henzel,W.J. and Vandlen,R.

IL-1H, an interleukin 1-related protein that binds IL-18

receptor/IL-1Rrp

JOURNAL Cytokine 13 (1), 1-7 (2001)

MEDLINE 21066552

PUBMED 11145836

REFERENCE	2	(bases 1 to 817)
AUTHORS	Pan, G., Baldwin, D.T. and Zhong, A.W.	
TITLE	Direct Submission	
JOURNAL	Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way, South San Francisco, CA 94080, USA	
FEATURES	Location/Qualifiers	
source	1..817	
	/organism="Homo sapiens"	
	/db_xref="taxon:9606"	
	73..729	
	/note="IL-1H: IL-1 family member; binds IL-18 receptor/IL-1Rrp; putative involvement in inflammation and immune responses"	
	/codon_start=1	
	/product="interleukin-1-related protein long isoform a"	
	/protein_id="AAG14420.1"	
	/db_xref="GI:10185736"	
	/translation="MSFVGENSGVKMGSEDEKDEPQCLEDPAGSPLEPGLPTMNFVHTSPKVKNLNPKFESIHQDQKVLVDSGNLIVAPDKYIRPELIFALASSLSASAEKSPILGLVSKGEFCLYCDKDKGSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMNLESAAHPGMWFICTSCNCNEPVYTDKFNKRKHIEFSQPVCKAEMSPSEVSD"	
BASE COUNT	246 a	196 c 190 g 185 t
ORIGIN		
Query Match	88.6%;	Score 512.8; DB 9; Length 817;
Best Local Similarity	99.68;	Pred. No. 4e-148;
Matches 514; Conservative	0;	Mismatches 2; Indels 0; Gaps 0;
QY	64	AGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACAGATCAC 123
DB	214	ACAAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACAGATCAC 273
QY	124	AAAGTACTGTCTCTGACTCTGGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
DB	274	AAAGTACTGTCTCTGACTCTGGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 333
QY	184	CCAGAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGT 243
DB	334	CCAGAGATCTTCTTTCATTTAGCCTCATCTTGAGCTCAGCCTCTGCGGAGAAAGGAAGT 393
QY	244	CCGATTCTCTCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 303
DB	394	CCGATTCTCTCTGGGGGTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 453
QY	304	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTGCCCAAAG 363
DB	454	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTGCCCAAAG 513
QY	364	GAATCAGCAGCGCGGCCCTTCATCTTTATAGGCTCAGGTGGGCTCTGGAACATGCTG 423
DB	514	GAATCAGCAGCGCGGCCCTTCATCTTTATAGGCTCAGGTGGGCTCTGGAACATGCTG 573
QY	424	GAGTCGGCGGCTCAACCCCGATGTTTCATCTGCACCTCCTGCAATTTGATGAGCCTGTT 483
DB	574	GAGTCGGCGGCTCAACCCCGATGTTTCATCTGCACCTCCTGCAATTTGATGAGCCTGTT 633
QY	484	GGGGTGACAGATAATTGAGAACAGAAACACATTTGAATTTTCATTTCAACCAAGTTGC 543
DB	634	GGGGTGACAGATAATTGAGAACAGAAACACATTTGAATTTTCATTTCAACCAAGTTGC 693
QY	544	AAAGCTGAATGAGCCCCAGTGAGGTACGCGATTAG 579
DB	694	AAAGCTGAATGAGCCCCAGTGAGGTACGCGATTAG 729
RESULT 9		
LOCUS	AX133934	847 bp DNA linear PAT 15-MAY-2001
DEFINITION	Sequence 4 from Patent EP1092773.	
ACCESSION	AX133934	
VERSION	AX133934.1	GI:14139876
KEYWORDS		

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 847)
TITLE	Ushio,S., Nukada,Y., Yamamoto,K. and Kurimoto,M.
JOURNAL	Polypeptide and uses thereof
FEATURES	Patent: EP 1092773-A 4 18-APR-2001;
source	KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
	Location/Qualifiers
	1..847
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
BASE COUNT	244 a 210 c 202 g 191 t
ORIGIN	
Query Match	88.6%; Score 512.8; DB 6; Length 847;
Best Local Similarity	99.6%; Pred. No. 4.1e-148;
Matches 514; Conservative	0; Mismatches 2; Indels 0; Gaps 0
QY	64 AGAGTCCAAAGGTGAGAAGCTTAAACCCGAAGAAATTTCAGCATTCATGACGATCAC 123
Db	262 ACAAGTCCAAAGGTGAGAAGCTTAAACCCGAAGAAATTTCAGCATTCATGACGATCAC 321
QY	124 AAAGTACTGCTCTGACTCTGGGAAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
Db	322 AAAGTACTGCTCTGACTCTGGGAAATCTCATAGCAGTTCCAGATAAAACTACATACGC 381
QY	184 CCAGAGATCTTCTTTGCATTTAGCCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAAGAAGT 243
Db	382 CCAGAGATCTTCTTTGCATTTAGCCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAAGAAGT 441
QY	244 CCGATTCTCCTGGGGGTCTCTAAGGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 303
Db	442 CCGATTCTCCTGGGGGTCTCTAAGGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 501
QY	304 CAAAGTCATCCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTGGCTGCCCAAAAG 363
Db	502 CAAAGTCATCCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTGGCTGCCCAAAAG 561
QY	364 GAATCAGCAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTGGAACATGCTG 423
Db	562 GAATCAGCAGCGCGGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTGGAACATGCTG 621
QY	424 GAGTCGGCGGCTCACCCCGGATGCTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTT 483
Db	622 GAGTCGGCGGCTCACCCCGGATGCTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTT 681
QY	484 GCGGTGACAGATAAATTTGAGAACAGGAAACACATTTGAATTTTCATTCAACCAGTTTGC 543
Db	682 GCGGTGACAGATAAATTTGAGAACAGGAAACACATTTGAATTTTCATTCAACCAGTTTGC 741
QY	544 AAAGCTGAATGAGCCCAAGTGAGGTCAGCGATTAG 579
Db	742 AAAGCTGAATGAGCCCAAGTGAGGTCAGCGATTAG 777
RESULT 10	
AX133936	
LOCUS	AX133936 855 bp DNA linear PAT 15-MAY-2001
DEFINITION	Sequence 6 from Patent EP1092773.
ACCESSION	AX133936
VERSION	AX133936.1 GI:14139877
KEYWORDS	
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	Ushio,S., Nukada,Y., Yamamoto,K. and Kurimoto,M.
TITLE	1 (bases 1 to 855)
JOURNAL	Polypeptide and uses thereof
	Patent: EP 1092773-A 6 18-APR-2001;
	KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)

FEATURES		Location/Qualifiers			
source		1..855	/organism="Homo sapiens"		
			/db_xref="taxon:9606"		
CDS		121..777	/note="unnamed protein product"		
			/codon_start=1		
			/protein_id="CAC38971.1"		
			/db_xref="GI:14139878"		
			/translation="MSFVGENSGVKMGSEDEKDEPQCCLEDPAVSPLEPQSLPAMN		
			FVHTSPKVKNLNPKKFSIHQDHLVLDGSLIAVPDKNYIRPEIFLASSLSAS		
			AEKGSPIILGVSKGEFLCYCDKDKGSHPSLQKKELMKLAQKESARPFIFYRAQ		
			VGSWMNLESAAHPGWFICTSCNENEPVGTDFENRKHIEFSFQPVCKAEMSPSEVSD		
BASE COUNT	252 a	210 c	202 g	191 t	
ORIGIN					
Query Match	88.6%;	Score 512.8;	DB 6;	Length 855;	
Best Local Similarity	99.6%;	Pred. No. 4.1e-148;			
Matches 514;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;	
QY	64	AGAGGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCAGATCAC	123		
Db	262	ACAAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACCAGATCAC	321		
QY	124	AAAGTACTGGTCTTGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC	183		
Db	322	AAAGTACTGGTCTTGACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGC	381		
QY	184	CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTCGGAGAAAGAAAGT	243		
Db	382	CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTCGGAGAAAGAAAGT	441		
QY	244	CCGATTCTCTGGGGGCTCTTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA	303		
Db	442	CCGATTCTCTGGGGGCTCTTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA	501		
QY	304	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	363		
Db	502	CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG	561		
QY	364	GAATCAGCAGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCCTGGAACATGCTG	423		
Db	562	GAATCAGCAGCCGCCCTTCATCTTTATAGGCTCAGGTGGGCTCCTGGAACATGCTG	621		
QY	424	GAGTCGGCGGCTCAGCCCGGATGGTTCACTGCACTCCTGCAATTGTAATGAGCCTGTT	483		
Db	622	GAGTCGGCGGCTCAGCCCGGATGGTTCACTGCACTCCTGCAATTGTAATGAGCCTGTT	681		
QY	484	GGGTGACAGATAAATTGAGAACAGAAACACATTGAATTTTCATTTCAACAGATTTC	543		
Db	682	GGGTGACAGATAAATTGAGAACAGAAACACATTGAATTTTCATTTCAACAGATTTC	741		
QY	544	AAAGCTGAATGAGCCCCAGTGAGGTGACGCATTAG	579		
Db	742	AAAGCTGAATGAGCCCCAGTGAGGTGACGCATTAG	777		
RESULT 11					
AX048211	AX048211	630 bp	DNA	linear	PAT 15-DEC-2000
DEFINITION	Sequence 51 from Patent WO0070049.				
ACCESSION	AX048211				
VERSION	AX048211.1 GI:11877001				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	Tang,Y.T., Yue,H., Lal,P., Burford,N., Bandman,O., Baughn,M.R., Azimzai,Y., Lu,D.A. and Patterson,C.				
AUTHORS	Extracellular signaling molecules				
TITLE					

JOURNAL	Patent: WO 0070049-A 51 23-NOV-2000;
FEATURES	Incyte Genomics, Inc. (US) Location/Qualifiers source 1. .630 /organism="Homo sapiens" /db_xref="taxon:9606" /note="Incyte ID No: 4365383CB1"
BASE COUNT	185 a 156 c 141 g 148 t
ORIGIN	.
Query Match	88.0%; Score 509.6; DB 6; length 630; Best Local Similarity 99.2%; Pred. No. 3.9e-147; Matches 512; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	64 AGAGGTCCAAGGTGAAGAAGCTTAACCCGGAAGAAATTCAGCATTCATGACCAGATCAC 123 Db 37 ACAAGTCAAGGTGAAGAGCTTAACCCGGAAGAAATTCAGCATTCATGACCAGATCAC 96
QY	124 AAAGTACTGGTCTTGACTCTGGGAATCTCATAGCAGTTCCAGATAAAAATACATACGC 183 Db 97 AAAGTACTGGTCTTGACTCTGGGAATCTCATAGCAGTTCCAGATAAAAATACATACGC 156
QY	184 CCAGATCTTCTTTGATTAGCCATCATCTTGAGCTCAGCCTCGCGAAGAAAGAGT 243 Db 157 CCAGATCTTCTTTGATTAGCCATCATCTTGAGCTCAGCCTCGCGAAGAAAGAGT 216
QY	244 CCGATTCTCTGGGGGTCTTAAGGGAGTTTTGTCTCTACTGTGACAAGATAAAGGA 303 Db 217 CCGATTCTCTGGGGGTCTTAAGGGAGTTTTGTCTCTACTGTGACAAGATAAAGGA 276
QY	304 CAAGTCAATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 363 Db 277 CAAGTCAATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 336
QY	364 GAATCAGCACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGGCTCCTGGAACATGCTG 423 Db 337 GAATCAGCACGCGCGCCCTTCATCTTTATAGGGCTCAGTGGGCTCCTGGAACATGCTG 396
QY	424 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTTGTAATGAGCCTGTT 483 Db 397 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTTGTAATGAGCCTGTT 456
QY	484 GGGGTGACAGATAAATTTGGAACAAGAAACACATTTGATTTTCATTTCAACCAAGTTTGC 543 Db 457 GGGGTGACAGATAAATTTGGAACAAGAAACACATTTGATTTTCATTTCAACCAAGTTTGC 516.
QY	544 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 579 Db 517 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 552
RESULT 12	
LOCUS	AX092410 754 bp DNA linear PAT 21-MAR-2001
DEFINITION	Sequence 141 from Patent WO0116318.
ACCESSION	AX092410
VERSION	AX092410.1 GI:13444519
KEYWORDS	.
SOURCE	human.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 754)
REFERENCE	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A., Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and Wood,W.I.
TITLE	Secreted and transmembrane polypeptides and nucleic acids encoding the same
JOURNAL	Patent: WO 0116318-A 141 08-MAR-2001; Genentech, Inc. (US)
FEATURES	location/Qualifiers 1. .754 /organism="Homo sapiens"

BASE COUNT 214 a 190 c 172 g 178 t
ORIGIN

Query Match 87.0%; Score 504; DB 6; Length 754;
Best Local Similarity 100.0%; Pred. No. 2.2e-145;
Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 GTGAAGACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCACAAGTACTGGTC 135
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DB 181 GTGAAGACTTAAACCCGAGAAATTCAGCATTCATGACGAGATCACAAGTACTGGTC 240
OY 136 CTGCACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGCCAGAGATCTTC 195
|||||
DB 241 CTGCACTCTGGGAATCTCATAGCAGTCCAGATAAAACTACATACGCCAGAGATCTTC 300
OY 196 TTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGATCCGATCTCCTG 255
|||||
DB 301 TTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGATCCGATCTCCTG 360
OY 256 GGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAAGACAAAGTATCCCA 315
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DB 361 GGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAAGACAAAGTATCCCA 420
OY 316 TCCCTCAGCTGAAGAAGAACTGATGAGCTGGCTGCCCAAAAGGAATCAGCACGC 375
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DB 421 TCCCTCAGCTGAAGAAGAACTGATGAGCTGGCTGCCCAAAAGGAATCAGCACGC 480
OY 376 CGGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTTGAAACATGCTGGAGTGGCGGCT 435
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DB 481 CGGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTTGAAACATGCTGGAGTGGCGGCT 540
OY 436 CACCCCGGATGGTTCATCTGCACCTCTGCAATTGTAATGAGCCTGTTGGGGTGACAGAT 495
|||||
DB 541 CACCCCGGATGGTTCATCTGCACCTCTGCAATTGTAATGAGCCTGTTGGGGTGACAGAT 600
OY 496 AAATTGAGAACAGGAACACATTGAATTTTCATTTCACACAGTTTGCAAGCTGAATG 555
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DB 601 AAATTGAGAACAGGAACACATTGAATTTTCATTTCACACAGTTTGCAAGCTGAATG 660
OY 556 AGCCCACTGAGGTGAGCGATTAG 579
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DB 661 AGCCCACTGAGGTGAGCGATTAG 684

RESULT 13
AF251120 537 bp mRNA linear PRI 03-MAY-2001
LOCUS AF251120
DEFINITION Homo sapiens interleukin-1-related protein short isoform mRNA,
complete cds; alternatively spliced.
ACCESSION AF251120
VERSION AF251120.1 GI:10185739
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 537)
AUTHORS Pan,G., Risser,P., Mao,W., Baldwin,D.T., Zhong,A.W., Filvaroff,E.,
Yansura,D., Lewis,L., Eigenbrot,C., Henzel,W.J. and Vandlen,R.
TITLE IL-1H, an interleukin 1-related protein that binds IL-18
receptor/IL-1Rrp
JOURNAL Cytokine 13 (1), 1-7 (2001)
MEDLINE 21066552
PUBMED 11145836
REFERENCE 2 (bases 1 to 537)
AUTHORS Pan,G., Baldwin,D.T. and Zhong,A.W.
TITLE Direct Submission
JOURNAL Submitted (03-APR-2000) Endocrinology, Genentech, Inc., 1 DNA Way,
South San Francisco, CA 94080, USA
FEATURES
source 1..537
/organism="Homo sapiens"

CDS
/db_xref="taxon:9606"
1..537

/note="IL-1H; IL-1 family member; binds IL-18
receptor/IL-1Rrp; putative involvement in inflammation and
immune responses"
/codon_start=1
/product="interleukin-1-related protein short isoform"
/protein_id="A014422.1"
/db_xref="GI:10185740"

BASE COUNT 141 a 129 c 142 g 125 t
ORIGIN

Query Match 68.5%; Score 396.6; DB 9; Length 537;
Best Local Similarity 96.7%; Pred. No. 5.4e-112;
Matches 405; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

OY 161 TTCAGATAAATACTACATACGCCAGAGATCTCTTGCAATTAGCCTCATCCTGAGCT 220
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DB 119 TCCCGCCGATGATTTTGTTCACACAAAGATCTTCTTGCAATTAGCCTCATCCTGAGCT 178
OY 221 CAGCCTCTGCGGAGAAAGGAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTTGTTC 280
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DB 179 CAGCCTCTGCGGAGAAAGGAAGTCCGATTTCTCTGGGGGTCTCTAAAGGGAGTTTGTTC 238
OY 281 TCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAAC 340
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DB 239 TCTACTGTGACAAGGATAAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAAAC 298
OY 341 TGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCGCGGCTTCATCTTTATAGGGCTC 400
|||||
DB 299 TGATGAAGCTGGCTGCCCAAAAGGAATCAGCACGCGCGGCTTCATCTTTATAGGGCTC 358
OY 401 AGTGGGCTCTGGAACATGCTGAGTGGCGGCTCACCCCGATGTTTCATCTGCACT 460
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DB 359 AGTGGGCTCTGGAACATGCTGAGTGGCGGCTCACCCCGATGTTTCATCTGCACT 418
OY 461 CCTGCAATTGTAATGAGCCTGTTGGGTGACAGATAAATTTGAGAAACAGAAACACATTG 520
|||||
DB 419 CCTGCAATTGTAATGAGCCTGTTGGGTGACAGATAAATTTGAGAAACAGAAACACATTG 478
OY 521 AATTTCATTCAACACAGTTTGCAAAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 579
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DB 479 AATTTCATTCAACACAGTTTGCAAAAGCTGAATGAGCCCAAGTGAGGTGAGCGATTAG 537

RESULT 14
AY071841 474 bp mRNA linear PRI 20-MAY-2002
LOCUS AY071841
DEFINITION Homo sapiens IL-1F7e (IL1F7) mRNA, complete cds, alternatively
spliced.
ACCESSION AY071841
VERSION AY071841.1 GI:19068185
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens.
REFERENCE 1 (bases 1 to 474)
AUTHORS Taylor,S.L., Renshaw,B.R., Garka,K.E., Smith,D.E. and Sims,J.E.
TITLE Genomic organization of the interleukin-1 locus
JOURNAL Genomics 79 (5), 726-733 (2002)
MEDLINE 21988051
PUBMED 11991723
REFERENCE 2 (bases 1 to 474)
AUTHORS Taylor,S.L., Renshaw,B.R., Garka,K.E., Smith,D.E. and Sims,J.E.
TITLE Direct Submission
JOURNAL Submitted (26-DEC-2001) Molecular Genetics, Immunex Corporation, 51
University Street, Seattle, WA 98101, USA
FEATURES
Location/Qualifiers


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source 1. .474
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        /db_xref="taxon:9606"
        /chromosome="2"
        /map="2q"
        1. .474
        /gene="IL1F7"
        1. .474
        /gene="IL1F7"
        /note="cytokine; alternatively spliced"
        /codon_start=1
        /product="IL-1F7e"
        /protein_id="AAL67154.1"
        /db_xref="GI:19068186"
        /translation="MSFVGENSGVKMGSEDMEKDEPOCCLEEIFFALASSUSASAEK
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        MNMLESAHPGMFICTSCNCPNEPVGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD"
BASE COUNT 126 a 104 c 130 g 114 t
ORIGIN

Query Match 68.0%; Score 394; DB 9; Length 474;
Best Local Similarity 100.0%; Pred. No. 3.4e-111;
Matches 394; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 186 AGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCGCGAGAAAGAAAGTCC 245
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Db 81 AGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCGCGAGAAAGAAAGTCC 140

QY 246 GATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGACA 305
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Db 141 GATTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGACA 200

QY 306 AAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAGGA 365
    |||||||
Db 201 AAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAGGA 260

QY 366 ATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGGA 425
    |||||||
Db 261 ATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTGGA 320

QY 426 GTCGGGGCTCACCCCGGATGTTTCACTGCACTCCTGCAATGTAATGAGCCTGTTGG 485
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Db 321 GTCGGGGCTCACCCCGGATGTTTCACTGCACTCCTGCAATGTAATGAGCCTGTTGG 380

QY 486 GGTGACAGATAAATTGAGAACAGAAACACATTGAATTTTCATTCAACCAAGTTGCAA 545
    |||||||
Db 381 GGTGACAGATAAATTGAGAACAGAAACACATTGAATTTTCATTCAACCAAGTTGCAA 440

QY 546 AGCTGAATGAGCCCCAGTGAGGTGACCGATTAG 579
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Db 441 AGCTGAATGAGCCCCAGTGAGGTGACCGATTAG 474

RESULT 15
AXI33932 575 bp DNA linear PAT 15-MAY-2001
LOCUS AXI33932
DEFINITION Sequence 2 from Patent EP1092773.
ACCESSION AXI33932
VERSION AXI33932.1 GI:14139874
KEYWORDS
SOURCE
ORGANISM
unidentified.
unclassified.
REFERENCE 1 (bases 1 to 575)
AUTHORS Ushio,S., Nukada,Y., Yamamoto,K. and Kurimoto,M.
TITLE Polypeptide and uses thereof
JOURNAL Patent: EP 1092773-A 2 18-APR-2001;
KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO (JP)
FEATURES
location/Qualifiers
1. .575
/organism="unidentified"
/db_xref="taxon:32644"
BASE COUNT 172 a 142 c 141 g 120 t
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ORIGIN

Query Match 53.7%; Score 310.8; DB 6; Length 575;
Best Local Similarity 99.4%; Pred. No. 2.7e-85;
Matches 312; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGACTTAACCCGAGAATAATTCAGCATTCATGACCAAGATCAC 123
    |||||||
Db 262 ACAAGTCCAAAGGTGAAGACTTAACCCGAGAATAATTCAGCATTCATGACCAAGATCAC 321

QY 124 AAAGTACTGGTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAAACTACATACGC 183
    |||||||
Db 322 AAAGTACTGGTCTGGACTCTGGGAATCTCATAGCAGTCCAGATAAAAACTACATACGC 381

QY 184 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCGCGAGAAAGGAAGT 243
    |||||||
Db 382 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCGCGAGAAAGGAAGT 441

QY 244 CCGATTCTCCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAAGGA 303
    |||||||
Db 442 CCGATTCTCCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAAGGA 501

QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 363
    |||||||
Db 502 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 561

QY 364 GAATCAGCACGCCG 377
    |||||||
Db 562 GAATCAGCACGCCG 575
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Search completed: May 3, 2003, 06:02:45
Job time : 1803 secs

XX Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus -
XX
PS Claim 1(a); Page 8; 87pp; English.

The present sequence is that of the coding region of cDNA encoding human interleukin-1 zeta (IL-1 zeta, see AA95297), a member of the IL-1 family. The sequence was deduced from EST IMAGE clone 1628791, which encodes a partial open reading frame, and from additional sequences obtained from PCR and 5' RACE reactions. IL-1 zeta mRNA is generated from exons 3-6 of the IL-1 zeta locus. The mRNA is expressed most strongly in the testis, prostate, colon, brain, placenta, lung, foetal liver and lymph node. The invention is directed to novel, purified and isolated IL-1 zeta, IL-1 zeta splice variants and Xrec2 polypeptides (see AA95297-301), the nucleic acids (see AAA27918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. IL-1 zeta nucleic acids are used to: to express IL-1 zeta polypeptides; as probes to identify nucleic acids encoding proteins of the IL-1 ligand family; to identify human chromosome 2; to map genes on chromosome 2; to identify genes associated with diseases, syndromes, or other conditions associated with chromosome 2, such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia or lymphoma, and tibial muscular dystrophy; as single-stranded sense or antisense oligonucleotides to inhibit expression of IL-1 zeta polypeptides; to help detect defective genes in an individual; and for gene therapy.

Query Match	100.0%;	Score 579;	DB 21;	Length 579;
Best Local Similarity	100.0%;	Pred. No. 2.6e-183;		
Matches 579; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	ATGTCAGGCTGTGATAGCAGGGAAACAGAAAACCAAGGAAGAACAAGCTTTAAGAACGC	60
Dd	1	ATGTCAGGCTGTGATAGGAGGGAAACAGAAAACCAAGGAAGAACAAGCTTTAAGAACGC	60
QY	61	TTAAGAGGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGCATTCATGACCAGAT	120
Dd	61	TTAAGAGGTCCAAAGGTGAAGAACTTAAACCGAAGAAATTCAGCATTCATGACCAGAT	120
QY	121	CACAAAGTACTGCTCTTGACTCTGGAAATCTCATAGCAGTTCAGATAAAAACTCATTA	180
Dd	121	CACAAAGTACTGCTCTTGACTCTGGAAATCTCATAGCAGTTCAGATAAAAACTCATTA	180
QY	181	CGCCCGAGAGATTCTTTTGACATTAGCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAGGA	240
Dd	181	CGCCCGAGAGATTCTTTTGACATTAGCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAGGA	240
QY	241	AGTCCGATTCTCTGGGGTCTCTAAAGGGAGTTTTGTCTCTACTGTGACAAGATAAA	300
Dd	241	AGTCCGATTCTCTGGGGTCTCTAAAGGGAGTTTTGTCTCTACTGTGACAAGATAAA	300
QY	301	GGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTGGCTGCCCAA	360
Dd	301	GGACAAAGTCATCCATCCCTTCAGCTGAAGAAGGAGAACTGATGAAGCTGGCTGCCCAA	360
QY	361	AAGGAATCAGCACGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATG	420
Dd	361	AAGGAATCAGCACGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATG	420
QY	421	CTGAGTGGCGGGCTCACCCCCGGATGTTTCATCTGCACCTCTGCAATTGTATGAGCCT	480
Dd	421	CTGAGTGGCGGGCTCACCCCCGGATGTTTCATCTGCACCTCTGCAATTGTATGAGCCT	480
QY	481	GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTTGAATTTTCAACCAAGTT	540
Dd	481	GTTGGGGTGACAGATAAATTTGAGAACAGGAAACACATTTGAATTTTCAACCAAGTT	540

QY	541	TGCAAAAGCTGAAATGAGCCCCAGTGAGGTGAGCGATTAG	579
Db	541	TGCAAAAGCTGAAATGAGCCCCAGTGAGGTGAGCGATTAG	579

RESULT 2	
AAA27921	
ID	AAA27921 standard; cDNA; 594 BP.

AC AAA27921;

DT 12-SEP-2000 (first entry)

DE Human interleukin-1 zeta splice variant TDZ.2 cDNA.

KW Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;

KW ectodermal dysplasia; wrinkly skin syndrome; leukaemia; lymphoma;

XX

XX

XX



XX

PR 10-NOV-1999; 99US-0164675.

PA (IMMV) IMMUNEX CORP.

PI Sims JE, Smith DE, Born TL;

DR WPT; 2000-442387/38.

XX

PT	TDZ1, TDZ2, TDZ3
1	1
2	2
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92	92
93	93
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99	99
100	100

insulin-dependent

PS Claim 1(a); Page 10; 87pp; English.

The present sequence is that of the coding region of cDNA encoding splice variant TDZ.2 (testis-derived zeta variant, see AAY95300) of human interleukin-1 zeta (IL-1 zeta). TDZ.2 mRNA is generated from exons 1, 4, 5 and 6 of the IL-1 zeta locus on chromosome 2, and the encoded protein is probably a functional IL-1 like molecule. TDZ.2 mRNA is expressed most strongly in the testis and bone marrow. The invention is directed to novel, purified and isolated IL-1 zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301), the nucleic acids (see AAA27918-22) encoding such polypeptides, processes for production of recombinant forms of such polypeptides, and their uses. TDZ.2 nucleic acids are used to: to express TDZ.2 polypeptides; as probes to identify nucleic acids encoding proteins of the IL-1 ligand family; to identify human chromosome 2; to map genes on chromosome 2; to identify genes associated with diseases, syndromes, or other conditions associated with chromosome 2, such as glaucoma, ectodermal dysplasia, insulin-dependent diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia or lymphoma, and tibial muscular dystrophy; as single-stranded sense or antisense oligonucleotides to inhibit expression of TDZ.2 polypeptides; to help detect defective genes in an individual; and for gene therapy.

5Q	Sequence	594 BP;	169 A;	133 C;	154 G;	138 T;	0 other;
	Query Match	89.4%;	Score	517.8;	DB	21;	Length 594;
	Best Local Similarity	99.6%;	Pred. NO.	8.5e-163;			
	Matches 519; Conservative	0;	Mismatches	2;	Indels	0;	Gaps 0;

QY	59	GCTTAAGAGGTCCTCAAAAGGTGAAGAACTTAAACCCGAAGAAATTGACATTGATGACAGG	118
Db	74	GCTTAGAAGGTCCTCAAAAGGTGAAGAACTTAAACCCGAAGAAATTGACATTGATGACAGG	133
QY	119	ATCACAAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAAAACTACA	178
Db	134	ATCACAAAGTACTGCTGCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAAAACTACA	193
QY	179	TACGCCAGAGATCTTCTTTGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGGAGAAG	238
Db	194	TACGCCAGAGATCTTCTTTGCATTAGCCTCATCTTGAGCTCAGCCTCTGCGGAGAAG	253
QY	239	GAAATCCGATTTCTCTCTGGGGGTCTTAAAGGGAGTTTGTCTTACTGTGACAAGATA	298
Db	254	GAAATCCGATTTCTCTCTGGGGGTCTTAAAGGGAGTTTGTCTTACTGTGACAAGATA	313
QY	299	AAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAACTGATGAAGCTGGCTGCC	358
Db	314	AAGGACAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAACTGATGAAGCTGGCTGCC	373
QY	359	AAAAGAAATCAGCAGCGCCGCCCTTCATCTTTATAGGGCTAGAGTGGGCTCCTGGAACA	418
Db	374	AAAAGAAATCAGCAGCGCCGCCCTTCATCTTTATAGGGCTAGAGTGGGCTCCTGGAACA	433
QY	419	TGCTGAGTCGCGCGGCTCACCCCGGATGTTTCATCTGACACCTCTGCAATTGTAATGAGC	478
Db	434	TGCTGAGTCGCGCGGCTCACCCCGGATGTTTCATCTGACACCTCTGCAATTGTAATGAGC	493
QY	479	CTGTTGGGGTGACAGATAAATTTGAGAAACAGGAAACACATTTGAAATTTTCATTCAACCG	538
Db	494	CTGTTGGGGTGACAGATAAATTTGAGAAACAGGAAACACATTTGAAATTTTCATTCAACCG	553
QY	539	TTTGCAAAAGCTGAATAGAGCCCGCAGTGAGGTCAGCGATTAG	579
Db	554	TTTGCAAAAGCTGAATAGAGCCCGCAGTGAGGTCAGCGATTAG	594

RESULT	3
ID	AAA51592
AC	AAA51592 standard; DNA; 650 BP.
DT	31-OCT-2000 (first entry)
DE	Human IL-1R1a fused to heterologous signal sequence.
KW	hIL-1RaI; human interleukin-1 receptor antagonist-1; IL-1Ip; osteopathic;
KW	interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW	anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW	dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.
OS	Homo sapiens.
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	10..621
FT	/tag= a
FT	10..54
FT	/tag= b
FT	55..78
FT	/tag= c
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FT	79..117
FT	/tag= d
FT	/note= "Encodes linker peptide"
FT	118..618
FT	/tag= e
FT	/product= hIL-1RaI
PX	WO200039297-A2.
PD	06-JUL-2000.

XX	22-DEC-1999;	99WO-US30720.
PF		
XX	23-DEC-1998;	98US-0113430.
PR	22-JAN-1999;	99US-0116843.
PR	13-APR-1999;	99US-0129122.
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Goddard A, Pan J;	
XX		
DR	WPI; 2000-452395/39.	
DR	P-PSDB; AAY96933.	
XX		
PT	Nucleic acids encoding interleukin-1-like polypeptides, useful for	
PT	preventing and treating e.g. inflammation, asthma and psoriasis	
XX		
PS	Claim 7; Fig 2; 143pp; English.	

CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-11p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-11p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-11p protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-11p expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.

Query Match	89.1%;	Score 516;	DB 21;	Length 650;
Best Local Similarity	100.0%;	Pred. No. 3.6e-162;		
Matches 516;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 64	AGAGGTCCTCAAGGTTGAAGACTTTAAACCCGGAAGAAATTCAGCATTTATGACCAAGATCAC	123		
Db 106	AGAGGTCCTCAAGGTTGAAGACTTTAAACCCGGAAGAAATTCAGCATTTATGACCAAGATCAC	165		
QY 124	AAAGTACTGGTCTTGAGCTCTGGGAATCTCATAGCAGTTCCAGATFAAAAACTACATACGC	183		
Db 166	AAAGTACTGGTCTTGAGCTCTGGGAATCTCATAGCAGTTCCAGATFAAAAACTACATACGC	225		
QY 184	CCAGAGATCTTCTTTGATATAGCCTCATCCTTGAGCTCAGCCTCTCGGAGAAAGGAAGT	243		
Db 226	CCAGAGATCTTCTTTGATATAGCCTCATCCTTGAGCTCAGCCTCTCGGAGAAAGGAAGT	285		
QY 244	CCGATTCTCCTGGGGGTCTTAAAGGGGAGTTTGTCTCTACTGTGACAAAGGATAAAGGA	303		
Db 286	CCGATTCTCCTGGGGGTCTTAAAGGGGAGTTTGTCTCTACTGTGACAAAGGATAAAGGA	345		
QY 304	CAAACTCATCCATCCCTTCAGCTGAAGAAAGGAAACGTATGAAGCTGGCTGCCCAAAAG	363		
Db 346	CAAACTCATCCATCCCTTCAGCTGAAGAAAGGAAACGTATGAAGCTGGCTGCCCAAAAG	405		
QY 364	GAATCAGCACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	423		
Db 406	GAATCAGCACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	465		
QY 424	GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCAACCTCTGCAATTTGTAATGAGCCTGTT	483		
Db 466	GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCAACCTCTGCAATTTGTAATGAGCCTGTT	525		
QY 484	GGGGTGACAGATAAATTTGAGAACAGGAAACACATTTGAATTTTCATTTCAACCAAGTTTGC	543		

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Db      526 GGGGTGACAGATAAATTGAGACAGGAACACATTTGATTTTCATTTCAACCAAGTTTGC 585
QY      544 AAAGCTGAATGAGCCCGAGTGAGTCAGCGATTAG 579
      |||||||
Db      586 AAAGCTGAATGAGCCCGAGTGAGTCAGCGATTAG 621

RESULT 4
AAAS1591
ID      AAAS1591 standard; DNA; 1006 BP.
XX
AC      AAAS1591;
XX
DT      31-OCT-2000 (first entry)
XX
DE      Human IL-1 receptor antagonist 1 related DNA.
XX
KW      hIL-1Ra1; human interleukin-1 receptor antagonist-1; IL-1lp; osteopathic;
KW      interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW      anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW      dermatological; immunomodulatory; gastrointestinal; gene therapy; ds.
XX
OS      Homo sapiens.
XX
FH      Key
FT      CDS      Location/Qualifiers
FT              103..936
FT              /*tag= a
FT      exon      103..180
FT              /*tag= b
FT      intron      180..432
FT              /*tag= c
FT      exon      433..933
FT              /*tag= d

WO200039297-A2.
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PD      06-JUL-2000.
XX
PF      22-DEC-1999; 99WO-US30720.
XX
PR      23-DEC-1998; 98US-0113430.
PR      22-JAN-1999; 99US-0116843.
PR      13-APR-1999; 99US-0129122.
XX
PA      (GETH ) GENENTECH INC.
XX
PI      Goddard A, Pan J;
XX
DR      WPI; 2000-452395/39.
DR      P-PSDB; AAY96931, AAY96932.
XX
PT      Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT      preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS      Example 1; Fig 1A-B; 143pp; English.
XX
CC      An isolated nucleic acid molecule encoding an interleukin-1-like
CC      polypeptide (IL-1lp) that retains one or more activities of the peptide
CC      from which it is derived, such as the IL-18R binding activity of a human
CC      interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC      nucleic acids may be used in molecular engineering applications, e.g.
CC      hybridization assays and chromosome and gene mapping studies, for
CC      recombinantly producing the IL-1lp polypeptide or for producing gene
CC      knock out animals to study the role of the protein in metabolism and
CC      disease processes (conversely, gene therapy protocols may be used to
CC      supplement a patients production of the polypeptide or to rectify
CC      mutations that lead to the production of in active peptides). The
CC      peptides produced may be used to screen for and produce modulators (e.g.
CC      antibodies) of IL-1lp protein expression and activity which may be use
CC      to treat disorders associated with inappropriate IL-1lp expression and
CC      activity, such as inflammatory disorders, asthma, arthritis,
CC      osteoarthritis, sepsis, acute lung injury, adult respiratory distress
```

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CC      syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC      psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ      Sequence 1006 BP; 289 A; 246 C; 241 G; 230 T; 0 other;

Query Match      89.1%; Score 516; DB 21; Length 1006;
Best Local Similarity 100.0%; Pred. No. 4.6e-162;
Matches 516; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      64 AGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACGAGATCAC 123
      |||||||
Db      421 AGAGTCCAAAGGTGAAGACTTAAACCCGAAGAAATTCAGCATTCATGACGAGATCAC 480
QY      124 AAAGTACTGCTCCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAAACTACATACGC 183
      |||||||
Db      481 AAAGTACTGCTCCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAAACTACATACGC 540
QY      184 CCAGAGATCTTCTTTGCAATTAGCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAAGGAAGT 243
      |||||||
Db      541 CCAGAGATCTTCTTTGCAATTAGCCTCATCCTTGAGCTCAGCCTCTGCCGAGAAAGGAAGT 600
QY      244 CCGATTCTCCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAAAGATAAAGGA 303
      |||||||
Db      601 CCGATTCTCCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAAAGATAAAGGA 660
QY      304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 363
      |||||||
Db      661 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 720
QY      364 GAATCAGCAGCGCCGCCCTTCATCTTTTAAGGGCTCAGGTGGGCTCTGGAACATGCTG 423
      |||||||
Db      721 GAATCAGCAGCGCCGCCCTTCATCTTTTAAGGGCTCAGGTGGGCTCTGGAACATGCTG 780
QY      424 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTTGAATGAGCCTGTT 483
      |||||||
Db      781 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTTGAATGAGCCTGTT 840
QY      484 GGGGTGACAGATAAATTGAGAACAGAAACACATTTGATTTTCATTTCAACCAAGTTTGC 543
      |||||||
Db      841 GGGGTGACAGATAAATTGAGAACAGAAACACATTTGATTTTCATTTCAACCAAGTTTGC 900
QY      544 AAAGCTGAATGAGCCCGAGTGAGTCAGCGATTAG 579
      |||||||
Db      901 AAAGCTGAATGAGCCCGAGTGAGTCAGCGATTAG 936

RESULT 5
AAA27920
ID      AAA27920 standard; cDNA; 657 BP.
XX
AC      AAA27920;
XX
DT      12-SEP-2000 (first entry)
XX
DE      Human interleukin-1 zeta splice variant TDZ.1 cDNA.
XX
KW      Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1;
KW      testis-derived zeta variant; chromosome 2; gene therapy; glaucoma;
KW      ectodermal dysplasia; wrinkly skin syndrome; leukaemia; lymphoma;
KW      insulin-dependent diabetes mellitus; tibial muscular dystrophy; ss.
XX
OS      Homo sapiens.
XX
PN      WO200036108-A2.
XX
PD      22-JUN-2000.
XX
PF      14-DEC-1999; 99WO-US29549.
XX
PR      14-DEC-1998; 98US-0112163.
PR      10-NOV-1999; 99US-0164675.
XX
PA      (IMMV ) IMMUNEX CORP.
```


XX PI Sims JE, Smith DE, Born TL;
XX DR WPI; 2000-442387/38.
DR P-PSDB; AAY95299.
XX
PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT identifying genes associated with diseases such as glaucoma, and
PT insulin-dependent diabetes mellitus
XX
PS Claim 1(a); Page 9-10; 87pp; English.
XX
CC The present sequence is that of the coding region of cDNA encoding
CC splice variant TDZ.1 (testis-derived zeta variant, see AAY95299) of
CC human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA is generated from
CC exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus on chromosome 2, and
CC the encoded protein is probably a functional IL-1 like molecule.
CC TDZ.1 mRNA is expressed most strongly in the kidney, skeletal
CC muscle, testis, prostate, ovary, colon, small intestine, liver,
CC placenta, lung, tonsil, foetal liver, lymph node and bone marrow.
CC The invention is directed to novel, purified and isolated IL-1
CC zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301),
CC the nucleic acids (see AAA27918-22) encoding such polypeptides,
CC processes for production of recombinant forms of such polypeptides,
CC and their uses. TDZ.1 nucleic acids are used to: to express TDZ.1
CC polypeptides; as probes to identify nucleic acids encoding
CC proteins of the IL-1 ligand family; to identify human chromosome 2;
CC to map genes on chromosome 2; to identify genes associated with
CC diseases, syndromes, or other conditions associated with chromosome
CC 2, such as glaucoma, ectodermal dysplasia, insulin-dependent
CC diabetes mellitus, wrinkly skin syndrome, T-cell leukaemia or
CC lymphoma, and tibial muscular dystrophy; as single-stranded sense
CC or antisense oligonucleotides to inhibit expression of TDZ.1
CC polypeptides; to help detect defective genes in an individual; and
CC for gene therapy.
XX
SQ Sequence 657 BP; 185 A; 158 C; 165 G; 149 T; 0 other;

Query Match 88.6%; Score 512.8; DB 21; Length 657;
Best Local Similarity 99.6%; Pred. No. 4.3e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCAGCATTCATGACCAGATCAC 123
DB 142 ACAAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCAGCATTCATGACCAGATCAC 201
QY 124 AAAGTACTGGTCTGGAAGTCTGGAATCTCATTAGCAGTTCAGATATAAACTACATACGC 183
DB 202 AAAGTACTGGTCTGGAAGTCTGGAATCTCATTAGCAGTTCAGATATAAACTACATACGC 261
QY 184 CCAGAGATCTTCTTGACATTAGCCTCATCCCTGAGCTCAGCCTCTGCGAGAAAGGAGT 243
DB 262 CCAGAGATCTTCTTGACATTAGCCTCATCCCTGAGCTCAGCCTCTGCGAGAAAGGAGT 321
QY 244 CCGATTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAAAGGATAAAGGA 303
DB 322 CCGATTCTCTGGGGGCTCTTAAAGGGAGTTTGTCTCTACTGTGACAAAGGATAAAGGA 381
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 363
DB 382 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 441
QY 364 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 423
DB 442 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 501
QY 424 GAGTCGGCGGCTCAACCCGGATGTTTCATCTGCACTCCTGCAATTTAATGAGCCTGTT 483
DB 502 GAGTCGGCGGCTCAACCCGGATGTTTCATCTGCACTCCTGCAATTTAATGAGCCTGTT 561
QY 484 GGGGTGACAGATAAATTGAGACAGGAACAACATGGAATTTTCATTCAACCAAGTTTGC 543
|||||

DB 562 GGGGTGACAGATAAATTGAGACAGGAACACATTTGAATTTTCATTTCACACCAATTTC 621
QY 544 AAAGCTGAATGAGCCCCAGTGAAGTCAAGCATTAG 579
DB 622 AAAGCTGAATGAGCCCCAGTGAAGTCAAGCATTAG 657

RESULT 6
ID AAA08513
AAA08513 standard; DNA; 657 BP.
XX
AC AAA08513;
XX
DT 19-JUL-2000 (first entry)
XX
DE Primate interleukin-1 like (IL-1-zeta) alternative coding sequence.
XX
KW Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
KW hypoglycemia; plasma iron; plasma zinc; acute liver response;
KW plasma copper; ss.
XX
OS Mammalia.
XX
PN WO200017363-A2.
XX
PD 30-MAR-2000.
XX
PE 17-SEP-1999; 99WO-US20868.
XX
PR 18-SEP-1998; 98US-0156966.
XX
PA (SCHE) SCHERING CORP.
XX
PI Timans JC;
XX
DR WPI; 2000-283588/24.
DR P-PSDB; AAY91885.
XX
PT New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
PT sequence
XX
PS Disclosure; Page 102-103; 110pp; English.
XX
CC The present sequence encodes a primate interleukin-1 like molecule,
CC designated IL-1-zeta. It is an alternative sequence to AAA08512,
CC perhaps an allelic variant. The specification claims an isolated or
CC recombinant polypeptide that: (a) specifically binds polyclonal
CC antibodies generated against at least a 12 consecutive amino acid segment
CC of IL-1-zeta (see AAY91884) or its allelic variant (see AAY91885); and
CC (b) comprises at least one sequence selected from: AAY91886-903 or
CC AAY91904-06. The preferred 12 consecutive amino acid segment is chosen
CC from AAY91907-18 or AAY91919-21. IL-1-zeta is likely to play a role in
CC systemic inflammatory reactions, such as fever, hypoglycemia, reduced
CC plasma iron and zinc, the acute response of the liver, and increase
CC plasma copper. IL-1-zeta binding compounds (comprising antigen binding
CC sites) and IL-1-zeta polypeptides are also useful for both diagnostic and
CC therapeutic purposes.
XX
SQ Sequence 657 BP; 184 A; 158 C; 166 G; 149 T; 0 other;

Query Match 88.6%; Score 512.8; DB 21; Length 657;
Best Local Similarity 99.6%; Pred. No. 4.3e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCAGCATTCATGACCAGATCAC 123
DB 142 ACAAGTCCAAAGGTGAAGAACTTAAACCCGAGAAATTTCAGCATTCATGACCAGATCAC 201
QY 124 AAAGTACTGGTCTGGAAGTCTGGAATCTCATTAGCAGTTCAGATATAAACTACATACGC 183
DB 202 AAAGTACTGGTCTGGAAGTCTGGAATCTCATTAGCAGTTCAGATATAAACTACATACGC 261
|||||


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QY 184 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAACT 243
      |||||||
Db 262 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAACT 321
QY 244 CCGATTCTCTGGGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 303
      |||||||
Db 322 CCGATTCTCTGGGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 381
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
      |||||||
Db 382 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 441
QY 364 GAATCAGACAGCCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 423
      |||||||
Db 442 GAATCAGACAGCCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 501
QY 424 GAGTCGGCGGCTCACCCCGGATGTTCTGCACTCCTGCAATTTGATGAGCCTGT 483
      |||||||
Db 502 GAGTCGGCGGCTCACCCCGGATGTTCTGCACTCCTGCAATTTGATGAGCCTGT 561
QY 484 GGGGTGACAGATAAATTGAGACAGAAACACATTTGATTTCAACCAAGTTTGC 543
      |||||||
Db 562 GGGGTGACAGATAAATTGAGACAGAAACACATTTGATTTCAACCAAGTTTGC 621
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAAGCATTTAG 579
      |||||||
Db 622 AAAGCTGAATGAGCCCCAGTGAGGTCAAGCATTTAG 657

RESULT 7
AAC66727
ID AAC66727 standard; cDNA; 802 BP.
XX AC AAC66727;
XX DT 13-FEB-2001 (first entry)
XX DE Human interleukin-1 homologue IL-1H4 coding sequence.
XX KW Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
XX KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
XX KW transplant rejection; graft versus host disease; infection; stroke;
XX KW ischaemia; acute respiratory disease; allergy; asthma; restenosis;
XX KW brain injury; AIDS; bone disease; osteoporosis; cancer;
XX KW congestive heart failure; atherosclerosis; Alzheimer's disease; ss.
XX OS Homo sapiens.
XX PN WO200063226-A1.
XX PD 26-OCT-2000.
XX PF 14-APR-2000; 2000WO-US10207.
XX PR 16-APR-1999; 99US-0293625.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Young PR, McDonnell PC;
XX DR WPI; 2000-687155/67.
XX DR P-PSDB; AAB28266.
XX PT Interleukin-1 homologue useful for treating conditions such as chronic
XX PT and acute inflammation, septicemia, autoimmune diseases ischemia, acute
XX PT respiratory disease, allergies, and asthma
XX PS Claim 2; Page 28; 30pp; English.
XX CC The present sequence is the coding sequence for human interleukin-1
XX CC homologue (IL-1H4). IL-1H4 is useful for treating conditions such as
XX CC chronic and acute inflammation, septicemia, autoimmune diseases (e.g.
XX CC inflammatory bowel disease, psoriasis, and arthritis), transplant
```

```
CC rejection, graft versus host disease, infection, stroke, ischaemia,
CC acute respiratory disease, allergies, asthma, restenosis, brain injury,
CC AIDS, bone diseases (e.g. osteoporosis), cancer, congestive heart
CC failure, atherosclerosis, and Alzheimer's disease, related to either an
CC excess of, or an under-expression of, IL-1H4 polypeptide activity.
XX SQ Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 other;

Query Match 88.6%; Score 512.8; DB 21; Length 802;
Best Local Similarity 99.6%; Pred. No. 4.8e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAGAACTTAACCCGAGAAATTCAGCATTCATGACCAGATCAC 123
      |||||||
Db 199 ACAAGTCCAAAGGTGAGAACTTAACCCGAGAAATTCAGCATTCATGACCAGATCAC 258
QY 124 AAAGTACTGGTCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAACTACATAGCC 183
      |||||||
Db 259 AAAGTACTGGTCTGAGCTCTGGGAATCTCATAGCAGTTCAGATAAACTACATAGCC 318
QY 184 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAACT 243
      |||||||
Db 319 CCAGAGATCTTCTTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAACT 378
QY 244 CCGATTCTCTGGGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 303
      |||||||
Db 379 CCGATTCTCTGGGGGCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGGATAAAGGA 438
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
      |||||||
Db 439 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 498
QY 364 GAATCAGACAGCCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 423
      |||||||
Db 499 GAATCAGACAGCCGCGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 558
QY 424 GAGTCGGCGGCTCACCCCGGATGTTCTGCACTCCTGCAATTTGATGAGCCTGT 483
      |||||||
Db 559 GAGTCGGCGGCTCACCCCGGATGTTCTGCACTCCTGCAATTTGATGAGCCTGT 618
QY 484 GGGGTGACAGATAAATTGAGACAGAAACACATTTGATTTCAACCAAGTTTGC 543
      |||||||
Db 619 GGGGTGACAGATAAATTGAGACAGAAACACATTTGATTTCAACCAAGTTTGC 678
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAAGCATTTAG 579
      |||||||
Db 679 AAAGCTGAATGAGCCCCAGTGAGGTCAAGCATTTAG 714

RESULT 8
AAF84120
ID AAF84120 standard; cDNA; 802 BP.
XX AC AAF84120;
XX DT 22-AUG-2001 (first entry)
XX DE Interleukin-1 homologue (IL-1H4) polypeptide encoding cDNA.
XX KW Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
XX KW immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV;
XX KW cerebroprotective; antiasthmatic; vasotrophic; vulnerary; osteopathic;
XX KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
XX KW gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS 58..714
XX FT sig_peptide /product= "IL-1H4"
XX FT 58..117
XX FT /*tag= b
```

FT mat_peptide 118..711
FT /*tag= c
XX PN WO200140247-A1.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US32521.
XX PR 01-DEC-1999; 99US-0452140.
XX PA (SMIK) SMITHKLINE BEECHAM CORP.
XX PI Kumar S, McDonnell PC, Young PR;
XX DR WPI; 2001-389949/41.
XX DR P-PSDB; AAB85136.
XX
PT Novel interleukin-1 homolog, IL-1H4, for treating chronic and acute
PT inflammation, septicemia, autoimmune diseases, transplant rejection,
PT graft versus host disease, stroke, ischemia, allergy and asthma -
XX
PS Examples; Page 29; 30pp; English.
XX
CC The invention provides an isolated interleukin-1 homologue, IL-1H4
CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
CC modulators are useful for treating chronic and acute inflammation,
CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
CC psoriasis and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
CC polynucleotides are useful as diagnostic reagents and for chromosome
CC identification. The present sequence represents the cDNA encoding the
CC IL-1H4 polypeptide of the invention.
XX
SQ Sequence 802 BP; 243 A; 190 C; 185 G; 184 T; 0 other;

Query Match 88.6%; Score 512.8; DB 22; Length 802;
Best Local Similarity 99.6%; Pred. No. 4.8e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGTGAAGACTTAACCCGAAGAATTCAGCATTCATGACCAGATCAC 123
DB 199 ACAAGTCCAAAGTGAAGACTTAACCCGAAGAATTCAGCATTCATGACCAGATCAC 258
QY 124 AAAGTACTGGTCTGGACTCTGGGAATCTCATAGCAGTCCAGATTAATACTACATACGC 183
DB 259 AAAGTACTGGTCTGGACTCTGGGAATCTCATAGCAGTCCAGATTAATACTACATACGC 318
QY 184 CCAGAGATCTTCTTTCATTAGCCTCATCCTTGAGCTCAGCCTGCGGAGAAAGGAAGT 243
DB 319 CCAGAGATCTTCTTTCATTAGCCTCATCCTTGAGCTCAGCCTGCGGAGAAAGGAAGT 378
QY 244 CCGATTCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGGA 303
DB 379 CCGATTCTCTGGGGGCTCTTAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGGA 438
QY 304 CAAAGTCAATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 363
DB 439 CAAAGTCAATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGGCTGCCCAAAG 498
QY 364 GAATCAGCAGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 423
DB 499 GAATCAGCAGCGCGGCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 558
QY 424 GAGTCGGCGGCTCAACCCCGATGTTCAATCTGCACCTCCTGCAATTTGATGAGCCTGTT 483
DB 559 GAGTCGGCGGCTCAACCCCGATGTTCAATCTGCACCTCCTGCAATTTGATGAGCCTGTT 618
QY 484 GGGGTGACAGATTAATTGAGAACAGGAACACATTTGAATTTTCATTTCACACAGTTTGC 543

Db 619 GGGGTGACAGATAAATTGAGAACAGGAACACATTTTCATTTCACACAGTTTGC 678
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTGACGCAATTAG 579
DB 679 AAAGCTGAATGAGCCCCAGTGAGGTGACGCAATTAG 714

RESULT 9
AAA51604
ID AAA51604 standard; DNA; 839 BP.
XX
AC AAA51604;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 1 V DNA.
XX
KW hIL-1Ra1v; human interleukin-1 receptor antagonist-1; IL-1lp;
KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 73..729
FT /*tag= a
FT /product= hIL-1Ra1v
FT /partial
XX
WO200039297-A2.
06-JUL-2000. 
22-DEC-1999; 99WO-US30720.
XX
XX 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
PI
XX
DR WPI; 2000-452395/39.
DR P-PSDB; AAY96940.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS Claim 7; Fig 19; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1lp) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1Ra1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1lp polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patients production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1lp protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-1lp expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX

Sequence 839 BP: 249 A; 202 C; 196 G; 192 T; 0 other;

Query Match	88.6%;	Score 512.8;	DB 21;	Length 839;
Best Local Similarity	99.6%;	Pred. No. 4.9e-161;		
Matches 514; Conservative	0;	Mismatches 2;	Indels 0;	

QY	64	AGAGGCTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACCAGATCAC	123
Db	214	ACAACTCCAAAGGTGAAGAACTTAAACCCGAGAAATTCAGCATTCATGACCAGATCAC	273
QY	124	AAAGTACTGGTCTCTGGACTCTGGGAATCTATAGCAGTTCCAGATAAAACTACATACGC	183
Db	274	AAAGTACTGGTCTCTGGACTCTGGGAATCTATAGCAGTTCCAGATAAAACTACATACGC	333
QY	184	CCAGAGATCTTCTTTTGCAATTAGCCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAAGT	243
Db	334	CCAGAGATCTTCTTTTGCAATTAGCCCTCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAAGT	393
QY	244	CCGATTCTCCTGGGGGCTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA	303
Db	394	CCGATTCTCCTGGGGGCTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA	453
QY	304	CAAAGTCAATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAG	363
Db	454	CAAAGTCAATCCATCCCTTCAGCTGAAGAAGGAGAAACTGATGAAGCTGGCTGCCCAAAG	513
QY	364	GAATCAGCACGCGCGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	423
Db	514	GAATCAGCACGCGCGCCCTTCATCTTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG	573
QY	424	GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTT	483
Db	574	GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTT	633
QY	484	GGGGTGACAGATAAATTGAGAACACGSAACACATTTGAATTTTCATTTCAACACAGTTTGC	543
Db	634	GGGGTGACAGATAAATTGAGAACACGSAACACATTTGAATTTTCATTTCAACACAGTTTGC	693
QY	544	AAAGCTGAATGAGCCCCCAGTGAGGTGACGGATTAG 579	
Db	694	AAAGCTGAATGAGCCCCCAGTGAGGTGACGGATTAG 729	

RESULT 10	
AAC85680	
ID AAC85680	standard; cDNA; 847 BP.

AC AAC85680;

DT 29-JUN-2001 (first entry)

DE CDNA encoding IL-1 related substance.

KW Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
KW natural killer activity; immune system; gene therapy;
KW immunodeficiency; ss.

KW immunodeficiency; ss.

05 Homo sapiens.

FH	Key	Location/Qualifiers
FT	CDS	121..777

EP1092773-A2.

PD 18-APR-2001.

PF 11-OCT-2000; 2000EP-0308948

PR 15-OCT-1999; 99JP-0294493.

PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

XX Ushio S, Nukada Y, Yamamoto K, Kurimoto M;
PI
XX
DR WPI: 2001-275206/29.
DR P-PSDB; AAB47186.

PT New human interleukin-1-related polypeptide and polynucleotide, useful
PT for gene therapy and in developing drugs as regulators of natural
PT killer activity, are capable of inhibiting natural killer activity -
XX
PS Claim 4; Page 13; 15pp; English.

CC This sequence encodes an interleukin-1 (IL-1)-related polypeptide.
CC IL-1 related polypeptide was isolated from HPB-MLR cells, FERM-BP-2430,
CC an established human T-cell line. IL-1 related polypeptide is useful
CC for inhibiting natural killer (NK) activity, which is related to the
CC immune system of mammals. The DNA encoding the IL-1 related polypeptide
CC is useful in gene therapy of patients in need of NK activity inhibition
CC and others suffering from immunodeficiency.

Sequence: 847 BP; 244 A; 210 C; 202 G; 191 T; 0 other;

Query Match	88.6%;	Score 512.8;	DB 22;	Length 847;
Best Local Similarity	99.6%;	Pred. No. 4.9e-161;		
Matches 514; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

[illegible]

QY 304 CAAGTCATCCATCCCTTCAGCTGAAGGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
|||||
Db 502 CAAAGTCATCCATCCCTTCAGCTGAAGGAGAGAAACTGATGAAGCTGGCTGCCAAAAG 561
|||||

QY 364 GAATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGAAACATGCTG 423
|||||
Db 562 GAATCAGACGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGAAACATGCTG 621
|||||

QY 424 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCTGCAATTGTAATGAGCCTGTT 483
|||||
Db 622 GAGTCGGCGGCTCACCCCGGATGGTTCATCTGCACCTCTGCAATTGTAATGAGCCTGTT 681

QY 484 GGGGTGACAGATAAATTTGAGAACAGGAACACATTTGAATTTTCATTTCAACCAGTTGC 543
|||||
Db 682 GGGGTGACAGATAAATTTGAGAACAGGAACACATTTGAATTTTCATTTCAACCAGTTGC 741
|||||

QY	544	AAAGCTGAATGAGCCCCAGTGAGGTGAGCGATTAG	579
Db	742	AAAGCTGAATGAGCCCCAGTGAGGTGAGCGATTAG	777

RESULT 11	
AAI71179	
ID	AAI71179 standard; cDNA; 1104 BP.

AC AAI71179;

DT 22-JAN-2002 (first entry)

Human Interleukin 1 family protein encoding cDNA SEQ ID NO:4.

```
KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
KM Identification; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 370..1026
FT /*tag= a
FT /product= "IL-1 family protein"
XX
XX JP2001231578-A.
XX
XX PD 28-AUG-2001.
XX
XX PF 07-DEC-2000; 2000JP-0372864.
XX
XX PR 09-DEC-1999; 99JP-0349780.
XX
XX PA (KYOW ) KYOWA HAKKO KOGYO KK.
XX
XX DR WPI; 2001-609968/70.
XX
XX DR P-PSDB; AAG68116.
XX
XX PT An IL-1 family protein, used for the development of diagnostic and
XX treatment agents -
XX
XX PS Claim 2; Page 31-32; 38pp; Japanese.
XX
XX CC The present sequence encodes a human interleukin 1 (IL-1) family
XX protein having a combining affinity to a receptor of a protein of
XX human IL-1 family higher than Tango-77. The protein is useful for the
XX development of diagnostic, treating and/or preventive agents for
XX various diseases.
XX
XX SQ Sequence 1104 BP; 328 A; 258 C; 255 G; 263 T; 0 other;

Query Match 88.6%; Score 512.8; DB 22; Length 1104;
Best Local Similarity 99.6%; Pred. No. 5.7e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 64 AGAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGATTTCAGCCAGATCAC 123
DB 511 ACAAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGATTTCAGCCAGATCAC 570
OY 124 AAAGTACTGTCCTGACTCTTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
DB 571 AAAGTACTGTCCTGACTCTTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 630
OY 184 CCAGAGATCTTCTTGCAATTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 243
DB 631 CCAGAGATCTTCTTGCAATTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 690
OY 244 CCGATTCTCTGGGGTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA 303
DB 691 CCGATTCTCTGGGGTCTCTAAAGGGGAGTTTGTCTCTACTGTGACAAGATAAAGA 750
OY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
DB 751 CAAAGTCATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTGGCTGCCAAAAG 810
OY 364 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423
DB 811 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 870
OY 424 GAGTCGGCGGCTCACCCCGGATGGTTCAATCTGCACCTCTGCAATTGTAATGAGCCTGTT 483
DB 871 GAGTCGGCGGCTCACCCCGGATGGTTCAATCTGCACCTCTGCAATTGTAATGAGCCTGTT 930
OY 484 GGGGTGACAGATAAATTGAGAACAGAGAAACACATGTAATTTTCATTTCAACCAAGTTTGC 543
DB 931 GGGGTGACAGATAAATTGAGAACAGAGAAACACATGTAATTTTCATTTCAACCAAGTTTGC 990
OY 544 AAAGCTGAATGAGCCCAAGTGAGTCAAGCATTAG 579
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Db 991 AAAGCTGAATGAGCCCAAGTGAGTCAAGCATTAG 1026
|||||

RESULT 12
AAD00210
ID AAD00210 standard; cDNA; 1600 BP.
XX
XX AAD00210;
AC
AC 05-SEP-2000 (first entry)
XX
XX DT
XX
XX DE Human zilla4 cDNA.
XX
XX KW Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic;
KW anti-human immunodeficiency virus; HIV; ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 847..1503
XX FT /*tag= a
XX FT /product= "Human zilla4 protein"
XX
XX PN WO200024899-A2.
XX
XX PD 04-MAY-2000.
XX
XX PF 27-OCT-1999; 99WO-US25038.
XX
XX PR 27-OCT-1998; 98US-0179614.
XX
XX PA (ZYMO ) ZYMOGENETICS INC.
XX
XX PI West RR, Sheppard PO, Gao Z;
XX
XX DR WPI; 2000-350740/30.
XX
XX DR P-PSDB; AAY70927.
XX
XX PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
XX treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
XX disease, leukemia -
XX
XX PS Example 2; Page 61-63; 88pp; English.
XX
XX CC The present cDNA sequence encodes human interleukin (IL)-1 homolog zilla4
XX protein. This cDNA was cloned from a human foetal lung cDNA library. The
XX zilla4 proteins modulate inflammation and other immunological
XX processes and are therefore useful for treatment of arthritis, psoriasis,
XX septic shock, graft-versus-host disease and leukaemia. Other diseases
XX that may be modulated by zilla4 proteins include cancer, anaemia,
XX inflammatory bowel disease, acute and chronic neuropathologies, shock,
XX respiratory disease syndrome, restenosis and acquired immune deficiency
XX syndrome.
XX
XX SQ Sequence 1600 BP; 481 A; 356 C; 378 G; 385 T; 0 other;

Query Match 88.6%; Score 512.8; DB 21; Length 1600;
Best Local Similarity 99.6%; Pred. No. 7e-161;
Matches 514; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 64 AGAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGATTTCAGCCAGATCAC 123
DB 988 ACAAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGATTTCAGCCAGATCAC 1047
OY 124 AAAGTACTGTCCTGACTCTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
DB 124 AAAGTACTGTCCTGACTCTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
```


Db 1048 AAGTACTGCTCTGAGCTCTGGGAATCTCATAGCAGTTCCAGATAAAAACTACATACGC 1107
QY 184 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 243
Db 1108 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 1167
QY 244 CCGATTTCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGCATAAAGGA 303
Db 1168 CCGATTTCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGCATAAAGGA 1227
QY 304 CAAAGTCATCCCTTCAGCTGAAGAGGAAACTGATGAAGCTGCTGCCAAAAG 363
Db 1228 CAAAGTCATCCCTTCAGCTGAAGAGGAAACTGATGAAGCTGCTGCCAAAAG 1287
QY 364 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 423
Db 1288 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGAACATGCTG 1347
QY 424 GAGTCGGGGCTCAGCCCGGATGTTTCATCTGCACTCTGCAATGTATGAGCCTGTT 483
Db 1348 GAGTCGGGGCTCAGCCCGGATGTTTCATCTGCACTCTGCAATGTATGAGCCTGTT 1407
QY 484 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCAATTCACAGCTTGC 543
Db 1408 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCAATTCACAGCTTGC 1467
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 579
Db 1468 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTAG 1503

RESULT 13
ID AAA51601 standard; DNA; 626 BP.

XX AAA51601;
AC AAA51601;

DT 31-OCT-2000 (first entry)

DE Human IL-1 receptor antagonist 1 long DNA.

XX hIL-1raIL; human interleukin-1 receptor antagonist-1 long; IL-1lp;
KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy; ds.

OS Homo sapiens.

XX Location/Qualifiers

FT CDS 4..626
FT /tag= a
FT /product= hIL-1raIL
FT /partial

PN WO200039297-A2.

PD 06-JUL-2000.

PF 22-DEC-1999; 99WO-US30720.

PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.

PA (GETH) GENENTECH INC.

PI Goddard A, Pan J;

DR WPI; 2000-452395/39.
DR P-PSDB; AAY96938.

PT Nucleic acids encoding interleukin-1-like polypeptides, useful for

PT preventing and treating e.g. inflammation, asthma and psoriasis
XX Claim 7; Fig 15; 143pp; English.
PS An isolated nucleic acid molecule encoding an interleukin-1-like
XX polypeptide (IL-1lp) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1raIL) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1lp polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1lp protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-1lp expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX Sequence 626 BP; 178 A; 154 C; 153 G; 141 T; 0 other;
SQ

Query Match 88.4%; Score 511.8; DB 21; Length 626;
Best Local Similarity 99.6%; Pred. No. 9e-161;
Matches 513; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGGTGAGAACTTAACCCGAGAAATTCAGATTCATGACCAGATCAC 123
Db 112 ACAAGTCCAAAGGTGAGAACTTAACCCGAGAAATTCAGATTCATGACCAGATCAC 171
QY 124 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 183
Db 172 AAAGTACTGCTCTGAGCTCTGGAATCTCATAGCAGTTCCAGATAAAACTACATACGC 231
QY 184 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 243
Db 232 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 291
QY 244 CCGATTTCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGA 303
Db 292 CCGATTTCTCTGGGGCTCTTAAGGGAGTTTGTCTCTACTGTGACAAGATAAGGA 351
QY 304 CAAAGTCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTGGCTGCCAAAAG 363
Db 352 CAAAGTCATCCCTTCAGCTGAAGAGGAGAAACTGATGAAGCTGGCTGCCAAAAG 411
QY 364 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 423
Db 412 GAATCAGCAGCCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCTGGAACATGCTG 471
QY 424 GAGTCGGGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATGTATGAGCCTGTT 483
Db 472 GAGTCGGGGCTCAGCCCGGATGTTTCATCTGACCTCTGCAATGTATGAGCCTGTT 531
QY 484 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCAATTCACAGCTTGC 543
Db 532 GGGGTGACAGATAATTGAGAACAGAAACACATTTGATTTTCAATTCACAGCTTGC 591
QY 544 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTGA 578
Db 592 AAAGCTGAATGAGCCCCAGTGAGGTCAGCGATTGA 626

RESULT 14
ID AAD00212 standard; cDNA; 657 BP.

XX AAD00212;

DT 05-SEP-2000 (first entry)

XX DE Human zilla4-E200K variant cDNA.
XX KW Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic;
KW anti-human immunodeficiency virus; HIV; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 1..657
FT . /*tag= a
FT unsure /product= "zilla4-E200K protein"
FT 598..600
FT /*tag= b
FT /product= "Encodes Lys"
PN WO200024899-A2.
XX PD 04-MAY-2000.
XX PF 27-OCT-1999; 99WO-US25038.
XX PR 27-OCT-1998; 98US-0179614.
XX PA (ZYMO) ZYMOGENETICS INC.
XX PI West RR, Sheppard PO, Gao Z;
XX DR WPI: 2000-350740/30.
DR P-PSDB; AAY70933.
XX PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia -
XX PS Disclosure; Page 76-77; 88pp; English.
XX CC The present cDNA sequence encodes a variant of human interleukin (IL)-1
CC homolog zilla4 protein designated zilla4-E200K. The replacement of
CC Glu (200) with Lys results in change in activity from agonist to
CC antagonist. The zilla4 proteins modulate inflammation and other
CC immunological processes and are therefore useful for treatment of
CC arthritis, psoriasis, septic shock, graft-versus-host disease and
CC leukaemia. Other diseases that may be modulated by zilla4 proteins
CC include cancer, anaemia, inflammatory bowel disease, acute and chronic
CC neuropathologies, shock, respiratory disease syndrome, restenosis and
CC acquired immune deficiency syndrome.
XX SQ Sequence 657 BP; 185 A; 158 C; 165 G; 148 T; 1 other;
Query Match 88.2%; Score 510.8; DB 21; Length 657;
Best Local Similarity 99.2%; Pred. No. 2e-160;
Matches 512; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 64 AGAGTCCAAAGTGAAGACTTAAACCCGAGAAGAAATTCAGCATTCATGACCAGATCAC 123
DB 142 ACAAGTCCAAAGTGAAGACTTAAACCCGAGAAGAAATTCAGCATTCATGACCAGATCAC 201
QY 124 AAAGTACTGGTCTGGACTCTGGGAATCTCATGACAGTTCAGATAAAAACTACATACGC 183
DB 202 AAAGTACTGGTCTGGACTCTGGGAATCTCATGACAGTTCAGATAAAAACTACATACGC 261
QY 184 CCAGAGATCTTCTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 243
DB 262 CCAGAGATCTTCTTGCATTAGCCTCATCCTTGAGCTCAGCCTCTGCGAGAAAGAGT 321
QY 244 CCAGATCTCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACCAAGATAAGGA 303

DB 322 CCGATTCCTCGGGGTCTCTAAAGGGAGGAGTTTGTCTCTACTGTGACACAGATAAAGGA 381
QY 304 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTGCCAAAG 363
DB 382 CAAAGTCATCCATCCCTTCAGCTGAAGAGAGAACTGATGAAGCTGGCTGCCAAAG 441
QY 364 GAATCAGCAGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGACATGCTG 423
DB 442 GAATCAGCAGCCGCCCTTCATCTTTATAGGGCTCAGGTGGGCTCCTGGACATGCTG 501
QY 424 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTGCAATTGATGAGCCTGTT 483
DB 502 GAGTCGGCGGCTCACCCCGGATGTTTCATCTGCACCTCTGCAATTGATGAGCCTGTT 561
QY 484 GGGTGACAGATAAATTGAGAACAGAAACACATTTGATTTCAACCAAGTTGC 543
DB 562 GGGTGACAGATAAATTGAGAACAGAAACACATTAARTTTTCATTTCAACCAAGTTGC 621
QY 544 AAAGCTGAATGAGCCCGAGTGAGTTCAGCGATTAG 579
DB 622 AAAGCTGAATGAGCCCGAGTGAGTTCAGCGATTAG 657
RESULT 15
AAC84317
ID AAC84317 standard; cDNA; 630 BP.
XX AC AAC84317;
XX DT 19-MAR-2001 (first entry)
XX DE Human EXCS encoding cDNA (clone ID 4365383CB1).
XX KW Extracellular signaling molecule; EXCS; anti-inflammatory; human;
KW immunosuppressive; cytostatic; neuroprotective; gastrointestinal;
KW virucide; antibacterial; anti-HIV; human immunodeficiency virus;
KW antifertility; cerebroprotective; nootropic; antiulcer; antifungal;
KW anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
KW keratolytic; protozoacide; gene therapy; ss.
XX OS Homo sapiens.
XX PN WO200070049-A2.
XX PD 23-NOV-2000.
XX PF 19-MAY-2000; 2000WO-US13975.
XX PR 19-MAY-1999; 99US-0134949.
PR 15-JUL-1999; 99US-0144270.
PR 30-JUL-1999; 99US-0146700.
PR 04-OCT-1999; 99US-0157508.
XX PA (INCY-) INCYTE GENOMICS INC.
XX PI Tang YT, Yue H, Lal P, Burford N, Bandman O, Baughn MR;
PI Azimzal Y, Lu DAM, Patterson C;
XX DR WPI: 2001-025021/03.
DR P-PSDB; AAB48081.
XX PT New human extracellular signaling nucleic acids and polypeptides useful
PT for diagnosing, treating and preventing infections and
PT gastrointestinal, neurological, reproductive, and
PT autoimmune/inflammatory disorders -
XX PS Claim 4; Page 112; 114pp; English.
XX CC The invention provides human extracellular signaling molecules (EXCS)
CC and polynucleotides which identify and encode EXCS. EXCS can be
CC expressed by standard recombinant methodology. The amino acid and nucleic
CC acid sequences of EXCS are useful for diagnosing, treating and

GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 3, 2003, 05:20:27 ; Search time 1503 Seconds
(without alignments)
6238.980 Million cell updates/sec

Title: US-09-876-790-1
Perfect score: 579
Sequence: 1 atgtcagcgtgtgtaggag.....ccagtgaggtcagcgattag 579

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues
Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estl:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	492	85.0	561	9	AI343258	AI343258 tb94b05.x
2	429.4	74.2	767	12	BG620449	BG620449 602617582
c 3	407	70.3	485	9	AI014548	AI014548 ou40f01.x
c 4	223.4	38.6	316	17	AQ041691	AQ041691 CIT-HSP-2
5	51.2	8.8	1219	11	AK009787	AK009787 Mus muscu
6	48.6	8.4	870	12	BF244205	BF244205 601863146

7	40.6	7.0	1051	11	AK009741	AK009741 Mus muscu
8	40.6	7.0	1199	11	AK008977	AK008977 Mus muscu
9	40.6	7.0	1531	11	AK010020	AK010020 Mus muscu
10	40.6	7.0	2843	11	AK014576	AK014576 Mus muscu
11	38.4	6.6	369	9	AI094892	AI094892 qa13f01.x
c 12	38.2	6.6	288	14	BQ479845	BQ479845 faa70g08.
c 13	37.8	6.5	436	10	AW361164	AW361164 RCI-CT025
c 14	37.8	6.5	539	10	AW368430	AW368430 CM3-HT019
c 15	37.8	6.5	555	10	AW361172	AW361172 RCI-CT025
c 16	37.8	6.5	555	12	BE695960	BE695960 RCI-CT025
c 17	37.8	6.5	557	10	AW368437	AW368437 CM3-HT019
c 18	37.4	6.5	230	14	BQ968703	BQ968703 QHB34O13.
c 19	37.4	6.5	524	17	AZ094009	AZ094009 RPCL-23-4
c 20	37	6.4	833	17	BH156690	BH156690 ENT5R5TF
21	36.8	6.4	373	9	AI401773	AI401773 lh23h05.x
22	36.8	6.4	379	10	AW043814	AW043814 wy81b09.x
23	36.8	6.4	454	9	AI275767	AI275767 qv67d07.x
c 24	36.6	6.3	469	14	BQ768134	BQ768134 EBR008-SQ
c 25	36.6	6.3	1020	12	BG245180	BG245180 602357579
c 26	36.4	6.3	375	9	AI220203	AI220203 qg84g07.x
27	36.2	6.3	348	9	AI141656	AI141656 ot08a05.x
28	36.2	6.3	406	17	AZ621717	AZ621717 1M0455A18
c 29	36.2	6.3	530	13	BM367565	BM367565 NXLV-051-
c 30	36.2	6.3	559	10	AW578451	AW578451 RCI-CT025
c 31	36.2	6.3	658	13	BI490370	BI490370 603031838
c 32	36.2	6.3	672	13	BI826186	BI826186 603076358
c 33	36	6.2	554	12	BG863310	BG863310 602798918
c 34	36	6.2	683	17	CNS04FGT	AL288326 Tetraodon
c 35	35.8	6.2	456	9	AI363086	AI363086 qy54g04.x
c 36	35.8	6.2	874	9	AU067032	AU067032 AU067032
c 37	35.4	6.1	380	17	BH449868	BH449868 BOGJL15TF
38	35.4	6.1	435	14	W78043	W78043 zd72d01.r1
39	35.4	6.1	442	9	AI863846	AI863846 wj54f08.x
40	35.4	6.1	578	17	BH714506	BH714506 BOHXP29TF
41	35.4	6.1	585	17	BH494058	BH494058 BOGZS38TF
c 42	35.4	6.1	593	17	BH481439	BH481439 BOHBL37TR
c 43	35.4	6.1	646	17	BH668410	BH668410 BOMES13TF
c 44	35.4	6.1	680	17	BH589224	BH589224 BOGVL33TF
c 45	35.4	6.1	683	17	BH546506	BH546506 BOGGG27TF

ALIGNMENTS

RESULT 1
AI343258/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI343258 561 bp mRNA linear EST 18-MAR-1999
tb94b05.x1 NCI_CGAP_Col6 Homo sapiens cDNA clone IMAGE:2061969 3',
mRNA sequence.
AI343258
AI343258.1 GI:4080464
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 561)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.
, Ph.D.

cdNA Library Preparation: M. Bento Soares, Ph.D.
cdNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert length: 814 Std Error: 0.00
Seq primer: -40UP from Gibco

High quality sequence stop: 471.
location/Qualifiers
1. 561
/organism="Homo sapiens"
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/clone="IMAGE:2061969"
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/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; plasmid DNA from the normalized library NCI_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneids 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 134 a 129 c 138 g 160 t
ORIGIN

Query Match 85.0%; Score 492; DB 9; Length 561;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 88 AACCCGAGAATTCAGCATTCATGACCAGATCACAAGTACTGTCCTGGACTGTGG 147
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Db 561 AACCCGAGAATTCAGCATTCATGACCAGATCACAAGTACTGTCCTGGACTGTGG 502

QY 148 AATCTCATGACAGTTCAGATAAAACTACATACGCCAGAGATCTTCTTGACATAGCC 207
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Db 501 AATCTCATGACAGTTCAGATAAAACTACATACGCCAGAGATCTTCTTGACATAGCC 442

QY 208 TCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAGTCCGATTCTCTGGGGTCTCTAAA 267
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Db 441 TCATCCTTGAGCTCAGCCTCTGCGGAGAAAGAGTCCGATTCTCTGGGGTCTCTAAA 382

QY 268 GGGGAGTTTGTCTCTACTGTGACAAGGATAAGGACAAAGTCAATCCCTTCAGCTG 327
|||||
Db 381 GGGGAGTTTGTCTCTACTGTGACAAGGATAAGGACAAAGTCAATCCCTTCAGCTG 322

QY 328 AAGAAGGAGAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCAGCCGCCCTTCATC 387
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Db 321 AAGAAGGAGAACTGATGAAGCTGGCTGCCCAAAAGGAATCAGCAGCCGCCCTTCATC 262

QY 388 TTTTATAGGGCTCAGGTGGCTCCTGGAACATGCTGAGTGGGGGCTCACCCCGGATGG 447
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Db 261 TTTTATAGGGCTCAGGTGGCTCCTGGAACATGCTGAGTGGGGGCTCACCCCGGATGG 202

QY 448 TTCATCTGCACCTCTCCTGCAATTTGAATGAGCCTGTGGGTTGACAGATAAATTGGAGAAC 507
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Db 201 TTCATCTGCACCTCTCCTGCAATTTGAATGAGCCTGTGGGTTGACAGATAAATTGGAGAAC 142

QY 508 AGGAAACACATGGAATTTTCATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCCAGTGAG 567
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Db 141 AGGAAACACATGGAATTTTCATTTCAACCAAGTTTGCAAAAGCTGAATGAGCCCCAGTGAG 82

QY 568 GTCAGCGATTAG 579
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Db 81 GTCAGCGATTAG 70

RESULT 2
Bg620449 767 bp mRNA linear EST 18-APR-2001
LOCUS 602617582F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4731213 5',
DEFINITION mRNA sequence.
ACCESSION Bg620449
VERSION Bg620449.1 GI:13671820
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 767)
AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: CLONTECH Laboratories, Inc.
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LICM1589 row: c column: 22
High quality sequence stop: 709.

FEATURES
source
location/Qualifiers
1. 767
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4731213"
/clone_lib="NIH_MGC_79"
/lab_host="DH10B (TI phage-resistant)"
/note="Organ: placenta; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgctggcc); Site_2: SfiI (ggccatattggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGAGCGGCCGACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

BASE COUNT 222 a 191 c 182 g 172 t
ORIGIN

Query Match 74.2%; Score 429.4; DB 12; Length 767;
Best Local Similarity 95.9%; Pred. No. 2e-113;
Matches 473; Conservative 0; Mismatches 16; Indels 4; Gaps 3;

QY 64 AGAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGCATTCATGACCAGATCAC 123
|||||
Db 146 ACAAGTCCAAAGGTGAAGAACTTAACCCGAGAATAATTCAGCATTCATGACCAGATCAC 205

QY 124 AAAGTACTGGTCTGGAAGTCTGGAATCTCATGACAGTTCCAGATAAAACTACATACGC 183
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Db 206 AAAGTACTGGTCTGGAAGTCTGGAATCTCATGACAGTTCCAGATAAAACTACATACGC 265

QY 184 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTGCGGAGAAAGAACT 243
|||||
Db 266 CCAGAGATCTTCTTTCATTTAGCCTCATCCTTGAGCTCAGCCTGCGGAGAAAGAACT 325

QY 244 CCGATTCTCTGGGGCTCTCTAAAGGGAGTTTGTCTCTACTGTGACAAGATAAGCA 303
|||||
Db 326 CCGATTCTCTGGGGCTCTCTAAAGGGAG-TTTGTCTCTACTGTGACAAGATAAGCA 384

QY 304 CAAAGTCAATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 363
|||||
Db 385 CAAAGTCAATCCATCCCTTCAGCTGAAGAAGAGAAACTGATGAAGCTGGCTGCCCAAAAG 444

QY 364 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGG-TGGGCTCCTGGAACATGCT 422
|||||
Db 445 GAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTTGGGCTCCTGGAACATGCT 504

QY 423 GGAGTCGGGGCTCACCCCGGATGGTTTCATCTGCACCTCTGCAATTTGTAATGAGCCTGT 482
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Db 505 GGAGTCGGAGGGTCAACCCGGATGGTTTCATCTGCACCTCTGCAATTTGTAATGAGCCTGT 564

QY 483 TGGGGTGACAGATAAATT--GAGAACAGGAACACATTTGAATTTTCATTTCAACCAAGTT 540
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Db 565 TGGGGTGACAGATAAATTTCGAGAACAGGAACACATTTGAATTTTCATTTCAACCAAGTT 624

QY 541 TGCAAAGCTGAAA 553
||||| |
Db 625 TGCAAAGGTTGAA 637

RESULT 3
AI014548/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

AI014548 485 bp mRNA linear EST 27-AUG-1998
ou40f01.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
IMAGE:1628761 3', mRNA sequence.
AI014548
AI014548.1 GI:3228929
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 485)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1052 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 424.
Location/Qualifiers
1. 485
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/db_xref="taxon:9606"
/clone="IMAGE:1628761"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."

BASE COUNT 117 a 112 c 119 g 137 t
ORIGIN

Query Match 70.3%; Score 407; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 5.5e-107;
Matches 407; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 ACTACATACGCCAGAGATCTTCTTGCACTAGCCCTCATCTGAGCTCAGCCTCTGCCG 232
|||||
Db 485 ACTACATACGCCAGAGATCTTCTTGCACTAGCCCTCATCTGAGCTCAGCCTCTGCCG 426

QY 233 AGAAGGAAGTCCGATTCCTCTGGGGGTCTTAAGGGAGTTTGTCTCTACTGTGACA 292
|||||
Db 425 AGAAGGAAGTCCGATTCCTCTGGGGGTCTCTAAAGGGAGTTTGTCTCTACTGTGACA 366

QY 293 AGGATTAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGG 352
|||||
Db 365 AGGATTAAGGACAAAGTCATCCATCCCTTCAGCTGAAGAGAGAAACTGATGAAGCTGG 306

QY 353 CTGCCCAAAAGGAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCT 412
|||||
Db 305 CTGCCCAAAAGGAATCAGCAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCT 246

QY 413 GGAACATGCTGGAGTGGCGGCTACCCCGGATGTTTCATCTGCACCTCCTGCAATTGTA 472
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Db 245 GGAACATGCTGGAGTGGCGGCTCACCCCGGATGTTTCATCTGCACCTCCTGCAATTGTA 186

QY 473 ATGAGCCTGTTGGGTGACAGATAAATTTGAGAACAGAAACACATTTGAATTTTCATTTC 532
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Db 185 ATGAGCCTGTTGGGTGACAGATAAATTTGAGAACAGAAACACATTTGAATTTTCATTTC 126

QY 533 AACCAATTGCAAAAGCTGAATGAGCCCCAGTGAGTCAAGCGATTAG 579
|||||
Db 125 AACCAATTGCAAAAGCTGAATGAGCCCCAGTGAGTCAAGCGATTAG 79

RESULT 4
AQ041691/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES

AQ041691 316 bp DNA linear GSS 14-JUL-1998
CIT-HSP-2326018.TR CIT-HSP Homo sapiens genomic clone 2326018, DNA
sequence.
AQ041691
AQ041691.1 GI:3310962
GSS.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 316)
Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
Unpublished (1998)
Other_GSSs: CIT-HSP-2326018.TV
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
Location/Qualifiers
1. 316
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/clone="2326018"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT 79 a 70 c 75 g 89 t 3 others
ORIGIN

Query Match 38.6%; Score 223.4; DB 17; Length 316;
Best Local Similarity 99.6%; Pred. No. 7.8e-54;
Matches 224; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 355 GCCCAAAAGGATCAGACAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTGG 414
|||||
Db 316 GCCCAAAAGGATCAGACAGCGCGCCCTTCATCTTTATAGGGCTCAGGTGGCTCCTGG 257

QY 415 AACATGCTGAGTGGCGGCTCACCCCGGATGTTTCATCTGCACCTCCTGCAATTTGTAAT 474
|||||
Db 256 AACATGCTGAGTGGCGGCTCACCCCGGATGTTTCATCTGCACCTCCTGCAATTTGTAAT 197

QY 475 GAGCCTGTTGGGTGACAGATAAATTTGAGAACAGAAACACATTTGAATTTTCATTTC 534
|||||
Db 196 GAGCCTGTTGGGTGACAGATAAATTTGAGAACAGAAACACATTTGAATTTTCATTTC 137

QY 535 CCAGTTTGAAGCTGAATGAGCCCCCAGTGAGGTGAGCGATTAG 579

TITLE	JOURNAL	MEDLINE	PUBMED	REFERENCE	AUTHORS
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system -384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res. 10 (11), 1757-1771 (2000)	20530913	11076861	4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED
4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gofjohori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaide, I., Pesole, G., Quackenbush, J., Schiml, L. M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamliya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Welter, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohatsu, S. and Hayashizaki, Y.	Functional annotation of a full-length mouse cDNA collection	Nature 409 (6821), 685-690 (2001)	21085660 11217851
5 (bases 1 to 1051)	Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A.,			

TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (<http://genome.gsc.riken.go.jp/>) for

cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cdNA was primed with a primer [5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cdNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cdNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cdNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAATTATCCCCCCCCCCC 3']. cdNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

FEATURES

Location/Qualifiers

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/strain="C57BL/6J"	
/db_xref="FANTOM_DB:2310041K07"	
/db_xref="MGD:MGI:1897667"	
/db_xref="taxon:10090"	
/clone="2310041K07"	
/sex="male"	
/tissue_type="tongue"	
/clone_lib="RIKEN full-length enriched mouse cDNA library"	
/dev_stage="adult"	
1. .1051	
/gene="Il1lf5"	
231. .701	
/gene="Il1lf5"	
/note="data source:MGD, source key:MGI:1859325, evidence:ISS interleukin 1 family, member 5 (delta) putative"	
/codon_start=1	
/protein_id="BAB26471.1"	
/db_xref="GI:12844720"	
/db_xref="MGD:MGI:1859325"	
/translation="MMVLGALCFRMKDSALKVLYLHNNQLAGLHAEKYIKGEIISVVPNRALDASLSPVILGVQGSQCLSCGTEKGPILKLEPVNIMELYLGAKESKSFTEYRRDMGLTSSFESEAAYPGWFLCTSP EADQPVRLTQIPEDPAWDAPITDFYQQCD"	

	Query Match	7.0%;	Score 40.6;	DB 11;	Length 1051;	
	Best Local Similarity	57.5%;	Pred. No. 1;			
Matches	73;	Conservative	0;	Mismatches	54;	Indels 0; Gaps 0;
QY	381	CTTCATCTTTATAGGGCTCAGGTGCGCTCCTTGAACATGCTGGAGTCGGGGCTACCC	440			
Db	524	CTTCACCTTCTACC GGCGGATATGGGCTTACCTCCAGCTTCAATCCGCTGCCTACCC	583			
QY	441	CGGATGGTTTCATCTGCACCTCCTGCAATTGTAATGAGCCTGTGGGGTGACAGATAAATT	500			
Db	584	AGGCTGGTTCTCTGCACCTCACCGGAAGCTGACCCAGCCTTCAGGCTCACTCAGATCCC	643			
QY	501	TGAGAAC	507			
Db	644	TGAGGAC	650			

RESULT 8	AK008977	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE
	AK008977	1199 bp	mRNA	linear	HTC 19-JAN-2002		
		Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2210418I04:interleukin 1 family, member 5 (delta), full insert sequence.					
	AK008977						
	AK008977.1	GI:12843490					
		HTC; CAP trapper.					
		Mus musculus (strain:C57BL/6J) adult male stomach cDNA to mRNA,					

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE	1
AUTHORS	Carninci, P. and Hayashizaki, Y.
TITLE	High-efficiency full-length cDNA cloning
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)
MEDLINE	99279253
PUBMED	10349636
REFERENCE	2
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)

REFERENCE	TITLE	JOURNAL	PUBMED	REFERENCE	TITLE	JOURNAL	PUBMED
2	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y. Normalization and subtraction of cap-trapped-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes	Genome Res.	10 (10), 1617-1630 (2000)	3	Shibata, K., Itoh, M., Alizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer	Genome Res.	10 (11), 1757-1771 (2000)
4	Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Stabli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bona, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Wilting, C., Wilting, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawai, J., Kohsaki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection	Nature	409 (6821), 685-690 (2001)				
	5 (bases 1 to 1531)						
	Adachi, J., Alizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Direct Submission						
	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)						
	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.						
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.						

division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5', GAGAGAGAGAAGGATCCACAGAGCTTTT TTTT TTTT TTTTN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 5.0 and subtraction to Rot = 25.0. Second strand cDNA was prepared with the primer adapter of sequence [5',

GAGAGAGAGATTCTCGAGTTAATTAAATAATCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

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FEATURES             location/Qualifiers
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                        /strain="C57BL/6J"
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                        /db_xref="MGI:1898160"
                        /db_xref="taxon:10090"
                        /clone="2310063B08"
                        /sex="male"
                        /tissue_type="tongue"
                        /clone_lib="RIKEN full-length enriched mouse cDNA library"
                        /dev_stage="adult"
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                    /gene="Il1f5"
misc_feature        1..1531
                    /note="data source:MGI, source key:MGI:1859325, evidence:ISS interleukin 1 family, member 5 (delta)"
                    /db_xref="MGI:1859325"
BASE COUNT          393 a      367 c      368 g      403 t
ORIGIN
Query Match         7.0%; Score 40.6; DB 11; Length 1531;
Best Local Similarity 57.5%; Pred. No. 1.2;
Matches 73; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY   381 CTTCACTTTTATAGGGCTCAGTGGGCTCCTGGAACATGTGGAGTCGGGCTCACCC 440
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Db   517 CTTCACCTTCTACCGCGGGGATATGGGCTCTTACCCTCCAGCTTGAATCCGCTGCCATCC 576

QY   441 CGGATGGTTCATCTGCACCTCCCTGCAATTGTAATGAGCCTGTGGGGTGACAGATAATT 500
      || ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   577 AGGCTGGTTCCTCTGCACCTCAACCGGAAGCTGACACAGCCTGTCAAGGCTCACTCAGATCCC 636

QY   501 TGAGAAC 507
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Db   637 TGAGGAC 643

RESULT 10
LOCUS   AK014576               2843 bp      mRNA       linear     HTC 19-JAN-2002
DEFINITION Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632413N13; Interleukin 1 family, member 5 (delta), full insert sequence.
VERSION AK014576
KEYWORDS AK014576.1 GI:12852516
SOURCE   HTC; CAP trapper.
          Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA to mRNA, clone_lib:RIKEN full-length enriched mouse cDNA library
          clone:4632413N13.
ORGANISM Mus musculus
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE
2

```


AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Akiyama,J., Nishi,K., Kitsuina,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I., Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Wittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsuki,S. and Hayashizaki,Y.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409 (6821), 685-690 (2001)
MEDLINE 21085660
PUBMED 11217851
REFERENCE 5 (bases 1 to 2843)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Baldarelli,R., Bono,H., Brownstein,M., Bult,C., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hill,D., Hiramoto,K., Hiraoka,T., Hori,F., Hume,D., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Quackenbush,J., Saito,H., Saito,R., Sakai,K., Sakai,K., Sano,H., Sasaki,D., Schriml,L., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yamanaka,I., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGCATCCAGAGCCTCTTTTTTT TTTT TTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCTCGAGTTAATTAAATTAAATCCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised between 3 and 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.
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Db 612 CTTCACTTTCTACCGCGGAGATAGGGCTTTACCTCCAGCTTCGAATCCGCTGACC 671
QY 441 CGAGTGTTCATCTGCACCTCTCGCAATTGTAATGAGCCTGTGGGTGACAGATAAATT 500
Db 672 AGGCTGTTCTCTGCACCTCACCAGCAAGCTGACACAGCTGTCAAGCTCACTCAGATCCC 731
QY 501 TGAGAAC 507
Db 732 TGAGGAC 738
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LOCUS ga13f01.x1 NCI_CGAP_Brn23 Homo sapiens cDNA clone IMAGE:1686649 3', mRNA sequence.
DEFINITION AI094892
ACCESSION AI094892
VERSION AI094892.1 GI:3433868
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 369)
AUTHORS NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTCAP), Tumor Gene Index
JOURNAL Unpublished (1998)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-r@mail.nih.gov
Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D., Ph.D.

FEATURES		Location/Qualifiers	
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ORIGIN			
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Best Local Similarity		52.1%; Pred. No. 5.6; Mismatches 117; Indels 6; Gaps 2;	
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QY	415	AACATGCTGAGTCGGGGCTCACCCTCGATGGTTCATCTGCACCTCCTGCAATTGTAAT	474
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QY	475	GAGCCTGTTGGGTGACAGATAAATTGAGACAGAAACACATTTGATTTTCAATTTCAA	534
Db	181	CAGCCCATCATTTCTGACTTCAGAACTTGGAGATCATACACACTGCTTTGAATTAAT	240
QY	535	CCAGTTTGCAAGCTGA	551
Db	241	ATAAATGACTGAACTCA	257

Search completed: May 3, 2003, 06:28:04
Job time : 1511 secs

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 3, 2003, 06:28:12 ; Search time 92 Seconds
(without alignments)
278.088 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRRETETKGKNSFKR.....IEFSFQPVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	100.0	192	21	AAV95297 Human interleukin-
2	906	89.1	203	21	AAV96933 Human IL-1R1a fuse
3	905	89.0	197	21	AAV95300 Human interleukin-
4	895	88.0	198	22	AAB85138 Interleukin-1 homo
5	895	88.0	207	21	AAV96938 Human IL-1 recepto
6	895	88.0	218	21	AAB28266 Human interleukin-
7	895	88.0	218	21	AAV96940 Human IL-1 recepto
8	895	88.0	218	21	AAV70927 Human zilla4 prote
9	895	88.0	218	21	AAV95299 Human interleukin-
10	895	88.0	218	21	AAV91885 Primate interleuki

11	895	88.0	218	22	AAG68116 Human interleukin
12	895	88.0	218	22	AAB85136 Interleukin-1 homo
13	895	88.0	218	22	AAB47186 IL-1 related polyp
14	892	87.7	218	21	AAV71084 Human zilla4-E200D
15	891	87.6	218	21	AAV70933 Human zilla4-E200K
16	885	87.0	193	21	AAV96934 Processed human IL
17	885	87.0	193	22	AAB87596 Human PRO3435. Ho
18	883	86.8	167	21	AAV96932 Human IL-1 recepto
19	883	86.8	176	22	AAB48081 Human extracellula
20	879	86.4	218	21	AAV70931 Human zilla4 varia
21	864	85.0	163	21	AAV97069 Human IL-1 recepto
22	859	84.5	218	21	AAV91884 Primate interleuki
23	775	76.2	218	21	AAV70928 Human zilla4 varia
24	704	69.2	167	21	AAV96939 Human IL-1 recepto
25	702	69.0	167	20	AAW93060 Human Tango-77 pro
26	702	69.0	178	20	AAW93057 Human Tango-77 pro
27	695	68.3	136	20	AAW93063 Human zilla4 splic
28	688	67.6	157	21	AAV70929 Human interleukin-
29	688	67.6	157	21	AAV95301 Human zilla4 varia
30	684	67.3	157	21	AAV70934 Human zilla4 varia
31	672	66.1	157	21	AAV70932 Human Tango-77 pro
32	623	61.3	115	20	AAW93059 Human Tango-77 mat
33	623	61.3	115	20	AAW93065 Human Tango-77 mat
34	618	60.8	114	20	AAW93062 Human IL-1 recepto
35	596	58.6	110	21	AAV97066 Human zilla4 varia
36	568	55.9	157	21	AAV70930 Human polypeptide
37	469	46.1	123	22	AAO04444 Human interleukin-
38	229	22.5	157	22	AAE04299 Human interleukin-
39	229	22.5	157	22	AAB50444 Human IL-1 eta. H
40	229	22.5	170	22	AAB85000 Human interleukin-
41	226.5	22.3	172	22	AAU17010 Human novel secret
42	226.5	22.3	172	22	AAE09702 Human gene 13 enco
43	225.5	22.2	169	19	AAW63136 Interleukin-1 rece
44	225.5	22.2	169	20	AAV24043 A human SPOIL-I pr
45	225.5	22.2	169	20	AAV24395 Human interleukin-

ALIGNMENTS

RESULT 1	
AAV95297	standard; Protein; 192 AA.
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AC	AAV95297;
XX	
DT	12-SEP-2000 (first entry)
XX	
DE	Human interleukin-1 zeta.
XX	
KW	Interleukin-1 zeta; IL-1 zeta; human; therapy; inflammation; fever.
XX	
OS	Homo sapiens.
XX	
PN	WO200036108-A2.
XX	
PD	22-JUN-2000.
XX	
PF	14-DEC-1999; 99WO-US29549.
XX	
PR	14-DEC-1998; 98US-0112163.
PR	10-NOV-1999; 99US-0164675.
XX	
PA	(IMMV) IMMUNEX CORP.
XX	
PI	Sims JE, Smith DE, Born TL;
XX	
DR	WPI; 2000-442387/38.
DR	N-PSDB; AAA27918.
XX	
PT	Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
PT	TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
PT	identifying genes associated with diseases such as glaucoma, and

PT Insulin-dependent diabetes mellitus -
XX
PS Claim 10; Page 8; 87pp; English.
XX
CC The present sequence is that of human interleukin-1 zeta (IL-1
CC zeta), a member of the IL-1 family. The sequence was determined
CC by translation of the nucleotide sequence of isolated IL-1 zeta
CC cDNA (see AAA27918). IL-1 zeta mRNA is generated from exons 3-6 of
CC the IL-1 zeta locus. The mRNA is expressed most strongly in the
CC testis, prostate, colon, brain, placenta, lung, foetal liver and
CC lymph node stroma, lung, testis and placenta. The invention is
CC directed to novel, purified and isolated IL-1 zeta, IL-1 zeta
CC splice variants and Xrec2 polypeptides (see AAY95297-301), the
CC nucleic acids (see AAA27918-22) encoding such polypeptides, processes
CC for production of recombinant forms of such polypeptides, and
CC their uses. The polypeptides can be used to study cellular
CC processes such as immune regulation, cell proliferation, cell
CC death, cell migration, cell-to-cell interaction and inflammatory
CC responses, to identify proteins associated with IL-1 zeta, to
CC screen for potential inhibitors, and to prepare antibodies. In
CC particular, they can be used to activate and/or inhibit the
CC activation of vascular endothelial cells and lymphocytes, induce
CC and/or inhibit the induction of local tissue destruction and fever,
CC inhibit and/or stimulate macrophages and vascular endothelial cells
CC to produce IL-6, induce and/or inhibit the induction of
CC prostaglandins, nitric oxide synthetase, and metalloproteinases, and
CC upregulate and/or inhibit the upregulation of molecules on the
CC surface of vascular endothelial cells.
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SQ Sequence 192 AA;

Query Match 100.0%; Score 1017; DB 21; Length 192;
Best Local Similarity 100.0%; Pred. No. 5.6e-111;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSGCDRRETETGKNSFKRRLGPKVKNLNPKKFSIHQDHKVLVDSGNLIAVPDKNYI 60
Db 1 MSGCDRRETETGKNSFKRRLGPKVKNLNPKKFSIHQDHKVLVDSGNLIAVPDKNYI 60

QY 61 RPEIFALASSLSASAEEKSPILLGVSGEFCLYCDKDGQSHPSQLKKEKIMKLAQ 120
Db 61 RPEIFALASSLSASAEEKSPILLGVSGEFCLYCDKDGQSHPSQLKKEKIMKLAQ 120

QY 121 KESARRPEIFYRAQVGSWNMLESAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSQPV 180
Db 121 KESARRPEIFYRAQVGSWNMLESAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSQPV 180

QY 181 CKAEMSPSEVSD 192
Db 181 CKAEMSPSEVSD 192

RESULT 2
AAY96933
ID AAY96933 standard; Protein; 203 AA.
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AC AAY96933;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1R1a fused to heterologous signal sequence.
XX
KW hIL-1R1; human interleukin-1 receptor antagonist-1; IL-11p; osteopathic;
KW interleukin-1-like polypeptide; anti-inflammatory; anti-asthmatic;
KW anti-arthritis; antimicrobial; respiratory; anti-ischemic; vaccine;
KW dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT Peptide /label= Signal_peptide
FT Peptide 16..23

FT FT /label= flag-tag
FT Peptide 24..36
FT /label= Linker
FT Protein 37..203
FT /label= hIL-1R1
XX
PN W0200039297-A2.
XX
PD 06-JUL-2000.
XX
PF 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI; 2000-452395/39.
DR N-PSDB; AAA51592.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS Claim 22; Fig 2; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-11p) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1R1) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-11p polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patient's production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-11p protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-11p expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
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SQ Sequence 203 AA;

Query Match 89.1%; Score 906; DB 21; Length 203;
Best Local Similarity 100.0%; Pred. No. 6.8e-98;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 RGPVKNLNPKKFSIHQDHKVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEEKS 81
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QY 82 PILLGVSGEFCLYCDKDGQSHPSQLKKEKIMKLAQKESARRPEIFYRAQVGSWNML 141
Db 93 PILLGVSGEFCLYCDKDGQSHPSQLKKEKIMKLAQKESARRPEIFYRAQVGSWNML 152

QY 142 ESAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSQPVCKAEMSPSEVSD 192
Db 153 ESAHPGWFICTSCNCPNPGVTDKFNKRKHIEFSQPVCKAEMSPSEVSD 203

RESULT 3
AAY95300
ID AAY95300 standard; Protein; 197 AA.
XX
AC AAY95300;
XX
DT 12-SEP-2000 (first entry)

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XX DE Human interleukin-1 zeta splice variant TDZ.2.
XX KW Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.2;
XX KW testis-derived zeta variant; therapy; inflammation; fever.
XX OS Homo sapiens.
XX PN WO200036108-A2.
XX PD 22-JUN-2000.
XX PF 14-DEC-1999; 99WO-US29549.
XX PR 14-DEC-1998; 98US-0112163.
XX PR 10-NOV-1999; 99US-0164675.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Sims JE, Smith DE, Born TL;
XX DR WPI: 2000-442387/38.
XX DR N-PSDB; AAA27921.
XX PT Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants
XX PT TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for
XX PT identifying genes associated with diseases such as glaucoma, and
XX PT insulin-dependent diabetes mellitus.
XX PS Claim 10; Page 11; 87pp; English.
XX CC The present sequence is that of splice variant TDZ.2 (testis-derived
XX CC zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.2 mRNA
XX CC is generated from exons 1, 4, 5 and 6 of the IL-1 zeta locus, and
XX CC the encoded protein is probably a functional IL-1 like molecule.
XX CC TDZ.2 mRNA is expressed most strongly in the testis and bone marrow.
XX CC The invention is directed to novel, purified and isolated IL-1
XX CC zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301),
XX CC the nucleic acids (see AAA27918-22) encoding such polypeptides,
XX CC processes for production of recombinant forms of such polypeptides,
XX CC and their uses. The polypeptides can be used to study cellular
XX CC processes such as immune regulation, cell proliferation, cell
XX CC death, cell migration, cell-to-cell interaction and inflammatory
XX CC responses, to identify proteins associated with IL-1 zeta, to
XX CC screen for potential inhibitors, and to prepare antibodies. In
XX CC particular, they can be used to activate and/or inhibit the
XX CC activation of vascular endothelial cells and lymphocytes, induce
XX CC and/or inhibit the induction of local tissue destruction and fever,
XX CC inhibit and/or stimulate macrophages and vascular endothelial cells
XX CC to produce IL-6, induce and/or inhibit the induction of
XX CC prostaglandins, nitric oxide synthetase, and metalloproteases, and
XX CC upregulate and/or inhibit the upregulation of molecules on the
XX CC surface of vascular endothelial cells.
XX SQ Sequence 197 AA;
Query Match 89.0%; Score 905; DB 21; Length 197;
Best Local Similarity 99.4%; Pred. No. 8.5e-98;
Matches 171; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 21 LRGPVKNLNPKKFSIHDDHKVLVLDSCNLIAYDPKNYIRPEIFFALASSLSASAEGK 80
Db 26 LEGPKVKNLNPKKFSIHDDHKVLVLDSCNLIAYDPKNYIRPEIFFALASSLSASAEGK 85
QY 81 SPILLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMN 140
Db 86 SPILLGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMN 145
QY 141 LESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 192
Db 146 LESAAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 197
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```
RESULT 4
AAB85138
ID AAB85138 standard; Protein; 198 AA.
XX AC AAB85138;
XX DT 22-AUG-2001 (first entry)
XX DE Interleukin-1 homologue (IL-1H4) mature polypeptide.
XX KW Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
XX KW immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV;
XX KW cerebroprotective; antiasthmatic; vasotropic; vulnerary; osteopathic;
XX KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
XX KW gene therapy; vaccine.
XX OS Homo sapiens.
XX PN WO200140247-A1.
XX PD 07-JUN-2001.
XX PF 30-NOV-2000; 2000WO-US32521.
XX PR 01-DEC-1999; 99US-0452140.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.
XX PI Kumar S, McDonnell PC, Young PR;
XX DR WPI: 2001-389949/41.
XX PT Novel Interleukin-1 homolog, IL-1H4, for treating chronic and acute
XX PT inflammation, septicemia, autoimmune diseases, transplant rejection,
XX PT graft versus host disease, stroke, ischemia, allergy and asthma.
XX PS Claim 1; Page 29; 30pp; English.
XX CC The invention provides an isolated interleukin-1 homologue, IL-1H4
XX CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
XX CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
XX CC modulators are useful for treating chronic and acute inflammation,
XX CC septicemia, autoimmune diseases (e.g., inflammatory bowel disease,
XX CC psoriasis and arthritis), transplant rejection, graft versus host
XX CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
XX CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
XX CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
XX CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
XX CC polynucleotides are useful as diagnostic reagents and for chromosome
XX CC identification. The present sequence represents the IL-1H4 mature
XX CC polypeptide.
XX SQ Sequence 198 AA;
```

Query Match 88.0%; Score 895; DB 22; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.3e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 24 PKVKNLNPKKFSIHDDHKVLVLDSCNLIAYDPKNYIRPEIFFALASSLSASAEGSPI 83
Db 30 PKVKNLNPKKFSIHDDHKVLVLDSCNLIAYDPKNYIRPEIFFALASSLSASAEGSPI 89
QY 84 ILGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 143
Db 90 ILGVSKGEFCLYCDKDGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 149
QY 144 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 192
Db 150 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSFQPVCKAEMSPSEVSD 198
```

RESULT 5
AAY96938

ID AAY96938 standard; Protein; 207 AA.
XX
AC AAY96938;
XX
DT 31-OCT-2000 (first entry)
XX
DE Human IL-1 receptor antagonist 1 long.
XX
KW hIL-1raIL; human interleukin-1 receptor antagonist-1 long; IL-1lp;
KW osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW anti-asthmatic; anti-arthritic; antimicrobial; respiratory; vaccine;
KW anti-ischemic; dermatological; immunomodulatory; gastrointestinal;
KW gene therapy.
XX
OS Homo sapiens.
XX
PN WO200039297-A2.
XX
PD 06-JUL-2000.
XX
PE 22-DEC-1999; 99WO-US30720.
XX
PR 23-DEC-1998; 98US-0113430.
PR 22-JAN-1999; 99US-0116843.
PR 13-APR-1999; 99US-0129122.
XX
PA (GETH) GENENTECH INC.
XX
PI Goddard A, Pan J;
XX
DR WPI; 2000-452395/39.
DR N-PSDB; AAA51601.
XX
PT Nucleic acids encoding interleukin-1-like polypeptides, useful for
PT preventing and treating e.g. inflammation, asthma and psoriasis
XX
PS Claim 22; Fig 15; 143pp; English.
XX
CC An isolated nucleic acid molecule encoding an interleukin-1-like
CC polypeptide (IL-1lp) that retains one or more activities of the peptide
CC from which it is derived, such as the IL-18R binding activity of a human
CC interleukin-1 receptor antagonist-1 (hIL-1raIL) polypeptide, is new. The
CC nucleic acids may be used in molecular engineering applications, e.g.
CC hybridization assays and chromosome and gene mapping studies, for
CC recombinantly producing the IL-1lp polypeptide or for producing gene
CC knock out animals to study the role of the protein in metabolism and
CC disease processes (conversely, gene therapy protocols may be used to
CC supplement a patients production of the polypeptide or to rectify
CC mutations that lead to the production of in active peptides). The
CC peptides produced may be used to screen for and produce modulators (e.g.
CC antibodies) of IL-1lp protein expression and activity which may be use
CC to treat disorders associated with inappropriate IL-1lp expression and
CC activity, such as inflammatory disorders, asthma, arthritis,
CC osteoarthritis, sepsis, acute lung injury, adult respiratory distress
CC syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease,
CC psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX
SQ Sequence 207 AA;

Query Match 88.0%; Score 895; DB 21; Length 207;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 PKVKNLNPKKFSIHQDQHKVLVLDSCNLIAYPPDKNYIRPEIFALASSLSASAEGSGPI 83
Db 39 PKVKNLNPKKFSIHQDQHKVLVLDSCNLIAYPPDKNYIRPEIFALASSLSASAEGSGPI 98
OY 84 LLGVSKEGFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMNLES 143
Db 99 LLGVSKEGFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMNLES 158
OY 144 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 192
|||||

Db 159 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 207
RESULT 6
ID AAB28266
XX AAB28266 standard; Protein; 218 AA.
AC AAB28266;
XX
DT 13-FEB-2001 (first entry)
XX
DE Human interleukin-1 homologue IL-1H4.
XX
KW Human; interleukin-1 homologue; IL-1H4; inflammation; septicemia;
KW autoimmune disease; inflammatory bowel disease; psoriasis; arthritis;
KW transplant rejection; graft versus host disease; infection; stroke;
KW ischaemia; acute respiratory disease; allergy; asthma; restenosis;
KW brain injury; AIDS; bone disease; osteoporosis; cancer;
KW congestive heart failure; atherosclerosis; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200063226-A1.
XX
PD 26-OCT-2000.
XX
PE 14-APR-2000; 2000WO-US10207.
XX
PR 16-APR-1999; 99US-0293625.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Young PR, McDonnell PC;
XX
DR WPI; 2000-687155/67.
DR N-PSDB; AAC66727.
XX
PT Interleukin-1 homolog useful for treating conditions such as chronic
PT and acute inflammation, septicemia, autoimmune diseases ischemia, acute
PT respiratory disease, allergies, and asthma
XX
PS Claim 1; Pages 28-29; 30pp; English.
XX
CC The present sequence is human interleukin-1 homologue (IL-1H4). IL-1H4 is
CC useful for treating conditions such as chronic and acute inflammation,
CC septicemia, autoimmune diseases (e.g. inflammatory bowel disease,
CC psoriasis, and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischaemia, acute respiratory disease,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.
CC osteoporosis), cancer, congestive heart failure, atherosclerosis, and
CC Alzheimer's disease, related to either an excess of, or an
CC under-expression of, IL-1H4 polypeptide activity.
XX
SQ Sequence 218 AA;

Query Match 88.0%; Score 895; DB 21; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 PKVKNLNPKKFSIHQDQHKVLVLDSCNLIAYPPDKNYIRPEIFALASSLSASAEGSGPI 83
Db 50 PKVKNLNPKKFSIHQDQHKVLVLDSCNLIAYPPDKNYIRPEIFALASSLSASAEGSGPI 109
OY 84 LLGVSKEGFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMNLES 143
Db 110 LLGVSKEGFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMNLES 169
OY 144 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCPNPGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 218
RESULT 7

AA96940	ID	AA96940 standard; Protein; 218 AA.
XX	AC	AA96940;
XX	DT	31-OCT-2000 (first entry)
XX	DE	Human IL-1 receptor antagonist 1 V.
KW	KW	hIL-1RaIV; human interleukin-1 receptor antagonist-1; IL-1Ip; osteopathic; interleukin-1-like polypeptide; anti-inflammatory;
KW	KW	anti-asthmatic; anti-arthritis; antimicrobial; respiratory; vaccine; anti-ischemic; dermatological; immunomodulatory; gastrointestinal; gene therapy.
XX	OS	Homo sapiens.
XX	PN	WO200039297-A2.
XX	PD	06-JUL-2000.
XX	PF	22-DEC-1999; 99WO-US30720.
XX	PR	23-DEC-1998; 98US-0113430.
PR	PR	22-JAN-1999; 99US-0116843.
PR	PR	13-APR-1999; 99US-0129122.
XX	PA	(GETH) GENENTECH INC.
XX	PI	Goddard A, Pan J;
XX	DR	WPI; 2000-452395/39.
DR	DR	N-PSDB; AAA51604.
XX	PT	Nucleic acids encoding interleukin-1-like polypeptides, useful for preventing and treating e.g. inflammation, asthma and psoriasis
XX	PS	Claim 22; Fig 19; 143pp; English.
XX	CC	An isolated nucleic acid molecule encoding an interleukin-1-like polypeptide (IL-1Ip) that retains one or more activities of the peptide from which it is derived, such as the IL-18R binding activity of a human interleukin-1 receptor antagonist-1 (hIL-1RaI) polypeptide, is new. The nucleic acids may be used in molecular engineering applications, e.g. hybridization assays and chromosome and gene mapping studies, for recombinantly producing the IL-1Ip polypeptide or for producing gene knock out animals to study the role of the protein in metabolism and disease processes (conversely, gene therapy protocols may be used to supplement a patients production of the polypeptide or to rectify mutations that lead to the production of in active peptides). The peptides produced may be used to screen for and produce modulators (e.g. antibodies) of IL-1Ip protein expression and activity which may be use to treat disorders associated with inappropriate IL-1Ip expression and activity, such as inflammatory disorders, asthma, arthritis, osteoarthritis, sepsis, acute lung injury, adult respiratory distress syndrome, idiopathic pulmonary fibrosis, ischemic reperfusion disease, psoriasis, graft versus host disease and/or inflammatory bowel disease.
XX	SQ	Sequence 218 AA;
QY	Query Match	88.0%; Score 895; DB 21; Length 218;
	Best Local Similarity	100.0%; Pred. No. 1.5e-96;
	Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	24	PKVKNLNPKKFSIHQDHRVVLVDSGNLIAVPDKNYIRPETIFALASSLSASAEGKSPI 83
Db	50	PKVKNLNPKKFSIHQDHRVVLVDSGNLIAVPDKNYIRPETIFALASSLSASAEGKSPI 109
QY	84	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 143
Db	110	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLES 169
QY	144	AAHPGWFICTSCNCNEPVGYTDFENRKHIEFSPQVPCKAEMSPSEVSD 192

Db	170	AAHPGWFICTSCNCPNPVGVTDKPFENRKHIIEFSFQPYCKAEMSPSEVSD	218	
RESULT 8				
AA70927	ID	AA70927	standard; Protein; 218 AA.	
XX	AC	AA70927;		
XX	DT	05-SEP-2000	(first entry)	
XX	DE	Human zilla4	protein.	
KW	KW	Human interleukin-1; IL-1; zilla4	protein; inflammation; arthritis	
KW	KW	psoriasis; septic shock; graft-versus-host	disease; leukaemia; ca	
KW	KW	anaemia; inflammatory bowel disease; acute	neuropathology; shock;	
KW	KW	chronic neuropathology; respiratory	disease syndrome; restenosis;	
KW	KW	acquired immune deficiency syndrome; AIDS;	antiinflammatory; cyto	
KW	KW	anti-arthritis; anti-psoriatic; antibacterial;	immunosuppressive;	
KW	KW	anti-anaemic; neuroprotective; vasotropic;		
KW	KW	anti-human immunodeficiency virus; HIV.		
XX	OS	Homo sapiens.		
XX	FH	Key	Location/Qualifiers	
FT	FT	Domain	60..64	/label= Beta_strand
FT	FT	Domain	68..72	/label= Beta_strand
FT	FT	Domain	77..79	/label= Beta_strand
FT	FT	Domain	90..96	/label= Beta_strand
FT	FT	Domain	108..113	/label= Beta_strand
FT	FT	Domain	118..123	/label= Beta_strand
FT	FT	Domain	132..138	/label= Beta_strand
FT	FT	Domain	154..160	/label= Beta_strand
FT	FT	Domain	165..169	/label= Beta_strand
FT	FT	Domain	175..179	/label= Beta_strand
FT	FT	Domain	187..189	/label= Beta_strand
FT	FT	Domain	201..204	/label= Beta_strand
FT	FT	Domain	65..67	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	73..76	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	80..89	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	97..107	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	114..117	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	124..131	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	139..153	/note= "Variable loop region involved in receptor binding"
FT	FT	Domain	161..164	/note= "Variable loop region involved in receptor binding"

[illegible]

KW	Interleukin-1 zeta; IL-1 zeta; splice variant; human; TDZ.1;	
KW	testis-derived zeta variant; therapy; inflammation; fever.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200036108-A2.	
XX		
PD	22-JUN-2000.	
XX		
PF	14-DEC-1999;	99WO-US29549.
XX		
PR	14-DEC-1998;	98US-0112163.
PR	10-NOV-1999;	99US-0164675.
XX		
PA	(IMMV) IMMUNEX CORP.	
XX		
PI	Sims JE, Smith DE, Born TL;	
XX		
DR	WPI; 2000-442387/38.	
DR	N-PSDB; AAA27920.	
XX		
PT	Isolated interleukin-1 (IL-1) zeta nucleic acids and splice variants	
PT	TDZ1, TDZ2, TDZ3 and their encoding proteins, useful as probes for	
PT	identifying genes associated with diseases such as glaucoma, and	
PT	insulin-dependent diabetes mellitus	
XX		
PS	Claim 10; Page 11; 87pp; English.	
XX		
CC	The present sequence is that of splice variant TDZ.1 (testis-derived	
CC	zeta variant) of human interleukin-1 zeta (IL-1 zeta). TDZ.1 mRNA	
CC	is generated from exons 1, 2, 4, 5 and 6 of the IL-1 zeta locus, and	
CC	the encoded protein is probably a functional IL-1 like molecule.	
CC	TDZ.1 mRNA is expressed most strongly in the kidney, skeletal	
CC	muscle, testis, prostate, ovary, colon, small intestine, liver,	
CC	placenta, lung, tonsil, foetal liver, lymph node and bone marrow.	
CC	The invention is directed to novel, purified and isolated IL-1	
CC	zeta, its splice variants and Xrec2 polypeptides (see AAY95297-301),	
CC	the nucleic acids (see AAA27918-22) encoding such polypeptides,	
CC	processes for production of recombinant forms of such polypeptides,	
CC	and their uses. The polypeptides can be used to study cellular	
CC	processes such as immune regulation, cell proliferation, cell	
CC	death, cell migration, cell-to-cell interaction and inflammatory	
CC	responses, to identify proteins associated with IL-1 zeta, to	
CC	screen for potential inhibitors, and to prepare antibodies. In	
CC	activation of vascular endothelial cells and lymphocytes, induce	
CC	and/or inhibit the induction of local tissue destruction and fever,	
CC	inhibit and/or stimulate macrophages and vascular endothelial cells	
CC	to produce IL-6, induce and/or inhibit the induction of	
CC	prostaglandins, nitric oxide synthetase, and metalloproteinases, and	
CC	upregulate and/or inhibit the upregulation of molecules on the	
CC	surface of vascular endothelial cells.	
XX		
SQ	Sequence	218 AA;
QY	Query Match	88.0%; Score 895; DB 21; Length 218;
	Best Local Similarity	100.0%; Pred. No. 1.5e-96;
	Matches 169; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Db	24	PKYKNLNPKKFSIHQDQHKVLYLDSGNLIAVPDKNYIRPEIFFALASSLSASAEKGSPI 83
Db	50	PKYKNLNPKKFSIHQDQHKVLYLDSGNLIAVPDKNYIRPEIFFALASSLSASAEKGSPI 109
QY	84	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKMLKLAQKESARPFIFYRAQGVSWNMLE 143
Db	110	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKMLKLAQKESARPFIFYRAQGVSWNMLE 169
QY	144	AAHPGWFICTSCNCPNCPVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 192
Db	170	AAHPGWFICTSCNCPNCPVGTDKFENRKHIEFSFQPVCKAEMSPSEVSD 218

AAV91885
ID AAY91885 standard; Protein; 218 AA.
XX
AC AAY91885;
XX
DT 19-JUL-2000 (first entry)
XX
DE Primate interleukin-1 like molecule (IL-1-zeta) alternative sequence.
XX
KW Primate; interleukin-1 like; IL-1-zeta; systemic inflammation; fever;
KW hypoglycemia; plasma iron; plasma zinc; acute liver response;
KW plasma copper.
XX
OS Mammalia.
XX
FH Key Location/Qualifiers
FT Domain 58..64
FT /label= beta_strand_1
FT 69..74
FT /label= beta_strand_2
FT 76..80
FT /label= beta_strand_3
FT 91..96
FT /label= beta_strand_4
FT 100..106
FT /note= "forms a loop which is part of a primary binding
FT segment to the IL-1 receptor type"
FT Domain 107..113
FT /label= beta_strand_5
FT 118..126
FT /label= beta_strand_6
FT 131..136
FT /label= beta_strand_7
FT 154..161
FT /label= beta_strand_8
FT 163..169
FT /label= beta_strand_9
FT 176..180
FT /label= beta_strand_10
FT 185..204
FT /label= beta_strand_11
FT 201..204
FT /label= beta_strand_12
XX
PN WO200017363-A2.
XX
PD 30-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US20868.
XX
PR 18-SEP-1998; 98US-0156966.
XX
PA (SCHE) SCHERING CORP.
XX
PI Timans JC;
XX
DR WPI; 2000-283588/24.
DR N-PSDB; AAA08513.
XX
PT New mammalian interleukin 1 like molecule, designated IL-1-zeta, useful
PT for diagnostic and therapeutic purposes, comprises a 128 amino acid
PT sequence
XX
PS Claim 1; Page 103-104; 110pp; English.
XX
CC The present sequence is an alternative primate interleukin-1 like
CC molecule, designated IL-1-zeta. The 12 beta strands, indicated in the
CC features table, fold into a beta-trefoil fold. The specification claims
CC an isolated or recombinant polypeptide that: (a) specifically binds
CC polyclonal antibodies generated against at least a 12 consecutive amino
CC acid segment of IL-1-zeta (see AAY91884) or its allelic variant (see
CC AAY91885); and (b) comprises at least one sequence selected from:
CC AAY91886-903 or AAY91904-06. The preferred 12 consecutive amino acid

CC segment is chosen from AAY91907-18 or AAY91919-21. IL-1-zeta is likely
CC to play a role in systemic inflammatory reactions, such as fever,
CC hypoglycemia, reduced plasma iron and zinc, the acute response of the
CC liver, and increase plasma copper. IL-1-zeta binding compounds
CC (comprising antigen binding sites) and IL-1-zeta polypeptides are also
CC useful for both diagnostic and therapeutic purposes.
XX
SQ Sequence 218 AA;
XX
Query Match 88.0%; Score 895; DB 21; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFFALASSLSASAEKGSPI 83
Db 50 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFFALASSLSASAEKGSPI 109
QY 84 LIGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMLES 143
Db 110 LIGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWMLES 169
QY 144 AAHPGWFICTSCNCNEPYGVTDKFEFNKRKHIEFSQFPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCNEPYGVTDKFEFNKRKHIEFSQFPVCKAEMSPSEVSD 218
RESULT 11
AAG68116
ID AAG68116 standard; Protein; 218 AA.
XX
AC AAG68116;
XX
DT 22-JAN-2002 (first entry)
XX
DE Human interleukin 1 family protein SEQ ID NO:2.
XX
KW Human; interleukin 1; IL-1; growth factor; Tango-77; diagnosis;
KW identification.
XX
OS Homo sapiens.
XX
PN JP2001231578-A.
XX
PD 28-AUG-2001.
XX
PF 07-DEC-2000; 2000JP-0372864.
XX
PR 09-DEC-1999; 99JP-0349780.
XX
PA (KYOW) KYOWA HAKKO KOGYO KK.
XX
DR WPI; 2001-609968/70.
DR N-PSDB; AA171179.
XX
PT An IL-1 family protein, used for the development of diagnostic and
PT treatment agents -
XX
PS Claim 1; Page 30; 38pp; Japanese.
XX
CC The present sequence represents a human interleukin 1 (IL-1) family
CC protein having a combining affinity to a receptor of a protein of
CC human IL-1 family higher than Tango-77. The protein is useful for the
CC development of diagnostic, treating and/or preventive agents for
CC various diseases.
XX
SQ Sequence 218 AA;
XX
Query Match 88.0%; Score 895; DB 22; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 PKYKLNLPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFFALASSLSASAEKGSPI 83
|||||

Db 50 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEGSGSPI 109
QY 84 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMLE 143
Db 110 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMLE 169
QY 144 AAHPGWFICTSCNCPNPVGVTDKFEENRKHIIEFSFQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCPNPVGVTDKFEENRKHIIEFSFQPVCKAEMSPSEVSD 218

RESULT 12

AAB85136

ID AAB85136 standard; Protein; 218 AA.

XX AC AAB85136;

DT 22-AUG-2001 (first entry)

DE Interleukin-1 homologue (IL-1H4) polypeptide.

XX Interleukin-1; IL-1H4; antiinflammatory; antibacterial; antiallergic;
KW immunosuppressive; antipsoriatic; antiarthritic; cytostatic; antiHIV;
KW cerebroprotective; antiasthmatic; vasotropic; vulnary; osteopathic;
KW immunostimulant; antiarteriosclerotic; nootropic; neuroprotective;
KW gene therapy; vaccine.

OS Homo sapiens.

XX Key Location/Qualifiers
FH Peptide 1..20
FT /note- "signal peptide"

FT Cleavage-site 20..21
FT Protein 21..218

/note- "specifically claimed mature protein (AAB85138)"

XX WO200140247-A1.

XX 07-JUN-2001.

XX 30-NOV-2000; 2000WO-US32521.

XX 01-DEC-1999; 99US-0452140.

XX (SMIK) SMITHKLINE BEECHAM CORP.

PI Kumar S, McDonnell PC, Young PR;

DR WPI; 2001-389949/41.

DR N-PSDB; AAF84120.

XX Novel interleukin-1 homolog, IL-1H4, for treating chronic and acute
PT inflammation, septiceamia, autoimmune diseases, transplant rejection,
PT graft versus host disease, stroke, ischemia, allergy and asthma
XX Examples; Page 29; 30pp; English.

XX The invention provides an isolated interleukin-1 homologue, IL-1H4
CC polypeptide. The IL-1H4 polypeptide can be expressed by standard
CC recombinant methodology. The IL-1H4 polypeptide, polynucleotides and
CC modulators are useful for treating chronic and acute inflammation,
CC septiceamia, autoimmune diseases (e.g., inflammatory bowel disease,
CC psoriasis and arthritis), transplant rejection, graft versus host
CC disease, infection, stroke, ischemia, acute respiratory disease syndrome,
CC allergies, asthma, restenosis, brain injury, AIDS, bone diseases (e.g.,
CC osteoporosis), cancer (e.g., lymphoproliferative disorders), congestive
CC heart failure, atherosclerosis and Alzheimer's disease. The IL-1H4
CC polynucleotides are useful as diagnostic reagents and for chromosome
CC identification. The present sequence represents the IL-1H4 polypeptide.

XX Sequence 218 AA;

Query Match 88.0%; Score 895; DB 22; Length 218;

Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEGSGSPI 83
Db 50 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEGSGSPI 109
QY 84 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMLE 143
Db 110 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMLE 169
QY 144 AAHPGWFICTSCNCPNPVGVTDKFEENRKHIIEFSFQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCPNPVGVTDKFEENRKHIIEFSFQPVCKAEMSPSEVSD 218

RESULT 13

AAB47186

ID AAB47186 standard; Protein; 218 AA.

XX AC AAB47186;

DT 29-JUN-2001 (first entry)

DE IL-1 related polypeptide.

XX Interleukin-1-related polypeptide; HPB-MLT cell; T-cell; inhibition;
KW natural killer activity; immune system; gene therapy;
KW immunodeficiency.

OS Homo sapiens.

XX EP1092773-A2.

XX 18-APR-2001.

XX 11-OCT-2000; 2000EP-0308948.

XX 15-OCT-1999; 99JP-0294493.

XX (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.

PI ushio S, Nukada Y, Yamamoto K, Kurimoto M;

DR WPI; 2001-275206/29.

DR N-PSDB; AAC85680.

XX New human interleukin-1-related polypeptide and polynucleotide, useful
PT for gene therapy and in developing drugs as regulators of natural
PT killer activity, are capable of inhibiting natural killer activity
XX Claim 1; Page 12; 15pp; English.

XX This sequence represents an interleukin-1 (IL-1)-related polypeptide.
CC IL-1 related polypeptide was isolated from HPB-MLT cells, FERM-BP-2430,
CC an established human T-cell line. IL-1 related polypeptide is useful
CC for inhibiting natural killer (NK) activity, which is related to the
CC immune system of mammals. The DNA encoding the IL-1 related polypeptide
CC is useful in gene therapy of patients in need of NK activity inhibition
CC and others suffering from immunodeficiency.

XX Sequence 218 AA;

Query Match 88.0%; Score 895; DB 22; Length 218;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEGSGSPI 83

Db 50 PKVKNLNPKKFSIHQDQHKVVLVDSGNLIAVPDKNYIRPEIFALASSLSASAEGSGSPI 109

QY 84 LGVSKGEFCLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMLE 143

|||||

Db 110 LLGVSKEFCLYCDKDGQSHPSLQLKKEKIMKLAQKESARRPFIIFYRAQVGSWMLES 169
QY 144 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQPVCKAEMSPSEVSD 218

RESULT 14
AAV71084

ID AAV71084 standard; Protein; 218 AA.

XX AAV71084;

DT 05-SEP-2000 (first entry)

DE Human zilla4-E200D variant protein.

XX Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic; variant;
KW anti-human immunodeficiency virus; HIV.

XX Homo sapiens.

PN WO200024899-A2.

PD 04-MAY-2000.

PF 27-OCT-1999; 99WO-US25038.

PR 27-OCT-1998; 98US-0179614.

PA (ZYMO) ZYMOGENETICS INC.

PI West RR, Sheppard PO, Gao Z;

DR WPI; 2000-350740/30.

PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia -
XX Claim 3; Page -: 88pp; English.

CC The present sequence is a variant of human interleukin (IL)-1
CC homolog zilla4 protein, consisting of Glu (200) with Asp results in
CC position 200. The replacement of Glu (200) with Asp results in
CC attenuation of pro-inflammatory activity of zilla4 protein.
CC The zilla4 proteins modulate inflammation and other
CC immunological processes and are therefore useful for treatment of
CC arthritis, psoriasis, septic shock, graft-versus-host disease and
CC leukaemia. Other diseases that may be modulated by zilla4 proteins
CC include cancer, anaemia, inflammatory bowel disease, acute and chronic
CC neuropathologies, shock, respiratory disease syndrome, restenosis and
CC acquired immune deficiency syndrome.
CC Note: The present sequence is not shown in the specification but is
CC derived from human zilla4 protein sequence shown in figure-2 (AAV70927).

SQ Sequence 218 AA;

Query Match 87.7%; Score 892; DB 21; Length 218;
Best Local Similarity 99.4%; Pred. No. 3.3e-96;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKNLNPKKFSIHQDHKVLVLDGSLIAVPDKNYIRPEIFALASSLSASAEKGSPI 83
Db 50 PKYKNLNPKKFSIHQDHKVLVLDGSLIAVPDKNYIRPEIFALASSLSASAEKGSPI 109
QY 84 LLGVSKEFCLYCDKDGQSHPSLQLKKEKIMKLAQKESARRPFIIFYRAQVGSWMLES 143

Db 110 LLGVSKEFCLYCDKDGQSHPSLQLKKEKIMKLAQKESARRPFIIFYRAQVGSWMLES 169
QY 144 AAHPGWFICTSCNCNEPVGVTDKFENRKHIEFSQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCNEPVGVTDKFENRKHIDFSQPVCKAEMSPSEVSD 218

RESULT 15
AAV70933

ID AAV70933 standard; Protein; 218 AA.

XX AAV70933;

DT 05-SEP-2000 (first entry)

DE Human zilla4-E200K variant protein.

XX Human interleukin-1; IL-1; zilla4 protein; inflammation; arthritis;
KW psoriasis; septic shock; graft-versus-host disease; leukaemia; cancer;
KW anaemia; inflammatory bowel disease; acute neuropathology; shock;
KW chronic neuropathology; respiratory disease syndrome; restenosis;
KW acquired immune deficiency syndrome; AIDS; antiinflammatory; cytostatic;
KW anti-arthritis; anti-psoriatic; antibacterial; immunosuppressive;
KW anti-anaemic; neuroprotective; vasotropic;
KW anti-human immunodeficiency virus; HIV.

XX Homo sapiens.

PN WO200024899-A2.

PD 04-MAY-2000.

PF 27-OCT-1999; 99WO-US25038.

PR 27-OCT-1998; 98US-0179614.

PA (ZYMO) ZYMOGENETICS INC.

PI West RR, Sheppard PO, Gao Z;

DR WPI; 2000-350740/30.

DR N-PSDB; AAD00212.

PT Immunomodulatory interleukin-1 homolog zilla4 proteins, useful for
PT treatment of e.g. arthritis, psoriasis, septic shock, graft-versus-host
PT disease, leukemia -
XX Claim 8; Page 77-78; 88pp; English.

CC The present sequence is a variant of human interleukin (IL)-1
CC homolog zilla4 protein designated zilla4-E200K. The replacement of
CC Glu (200) with Lys results in change in activity from agonist to
CC antagonist. The zilla4 proteins modulate inflammation and other
CC immunological processes and are therefore useful for treatment of
CC arthritis, psoriasis, septic shock, graft-versus-host disease and
CC leukaemia. Other diseases that may be modulated by zilla4 proteins
CC include cancer, anaemia, inflammatory bowel disease, acute and chronic
CC neuropathologies, shock, respiratory disease syndrome, restenosis and
CC acquired immune deficiency syndrome.

SQ Sequence 218 AA;

Query Match 87.6%; Score 891; DB 21; Length 218;
Best Local Similarity 99.4%; Pred. No. 4.3e-96;
Matches 168; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 24 PKYKNLNPKKFSIHQDHKVLVLDGSLIAVPDKNYIRPEIFALASSLSASAEKGSPI 83
Db 50 PKYKNLNPKKFSIHQDHKVLVLDGSLIAVPDKNYIRPEIFALASSLSASAEKGSPI 109
QY 84 LLGVSKEFCLYCDKDGQSHPSLQLKKEKIMKLAQKESARRPFIIFYRAQVGSWMLES 143

Db 110 LLGVSKEFCLYCDKDKGQSHPSLQLKKEKIMKLAQKESARRPFIYRAQVGSWNMLE 169
QY 144 AAHPGWFICTSCNCPVGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 192
Db 170 AAHPGWFICTSCNCPVGVTDKFEENRKHIEFSFQPVCKAEMSPSEVSD 218

Search completed: May 3, 2003, 18:34:24
Job time : 94 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:30:35 ; Search time 73 Seconds
(without alignments)
252.847 Million cell updates/sec

Title:	US-09-876-790-3
Perfect score:	1017
Sequence:	1 MSGCDRETETKGNPFKKR.....IEESFQPVCKAEMSPSEYSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing:	Minimum Match 0%
	Maximum Match 100%
	Listing first 45 summaries

```
Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	172.5	17.0	155	2	JC7104	interleukin-1 rece
2	159	15.6	178	2	A44610	interleukin-1 rece
3	151.5	14.9	177	2	A54377	interleukin-1 rece
4	150.5	14.8	180	2	A39386	interleukin-1 rece
5	149.5	14.7	177	2	A30368	interleukin-1 rece
6	144.5	14.2	178	2	C40956	interleukin-1 rece
7	127.5	12.5	266	1	S23010	interleukin-1 beta
8	119.5	11.8	267	1	JN0724	interleukin-1 beta
9	112.5	11.1	266	1	ICB01B	interleukin-1 beta
10	112.5	11.1	267	2	S38373	interleukin-1 beta
11	104	10.2	269	1	I55969	interleukin-1 beta
12	93	9.1	269	1	ICHU1B	interleukin-1 beta
13	91	8.9	404	2	S34031	KTR3 protein - yea
14	89.5	8.8	214	2	JC5646	interleukin-1 beta
15	89	8.8	268	1	A30584	interleukin-1 beta
16	84	8.3	270	1	ICMS1	interleukin-1 alph
17	81	8.0	776	2	S67053	probable membrane
18	80.5	7.9	571	2	D86164	hypothetical prote
19	80.5	7.9	845	2	T17291	hypothetical prote
20	80.5	7.9	3190	2	T13828	CREB-binding prote
21	79.5	7.8	1199	2	T15826	hypothetical prote
22	77	7.6	859	2	C87358	hypothetical prote
23	76.5	7.5	627	2	T02846	hypothetical prote
24	76	7.5	425	2	T24522	dynein light chain
25	76	7.5	448	2	JN0118	glucan 1,3-beta-gl
26	76	7.5	914	2	B96592	hypothetical prote
27	75	7.4	361	2	S23346	hypothetical prote
28	74.5	7.3	256	2	S37926	hypothetical prote
29	74.5	7.3	1151	2	T04657	hypothetical prote

30	74	7.3	545	2	T19172	hypothetical prote
31	74	7.3	803	2	E81804	hypothetical prote
32	74	7.3	1116	2	T14598	polyprotein - slim
33	73.5	7.2	460	2	T47709	glucuronosyl trans
34	73	7.2	201	2	E81309	nitroreductase Cj1
35	73	7.2	231	2	S59589	histone H1 - Chlam
36	73	7.2	317	2	AH0351	hypothetical prote
37	73	7.2	453	2	C90568	hypothetical prote
38	72.5	7.1	247	2	T50286	hypothetical prote
39	72.5	7.1	351	2	T19372	hypothetical prote
40	72.5	7.1	685	2	E82297	c-di-GMP phosphodi
41	72.5	7.1	933	2	G70166	probable zinc prot
42	72	7.1	307	2	E86323	protein F14D16.11
43	72	7.1	1034	2	B86880	SWI/SNF family hel
44	71.5	7.0	224	2	D90213	conserved hypothet
45	71.5	7.0	268	1	A61246	interleukin-1 alph

ALIGNMENTS

RESULT 1
JC7104
interleukin-1 receptor antagonist - human
C/Species: Homo sapiens (man)
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C/Accession: JC7104
R/Muetero, J.J.; Pace, A.M.; Nelken, S.T.; Loeb, D.B.; Correa, T.R.; Drmanac, R.; Fort
Biochem. Biophys. Res. Commun. 263, 702-706, 1999
A/Title: IL1HY1: A novel interleukin-1 receptor antagonist gene.
A/Reference number: JC7104; MUID:99443727; PMID:10512743
A/Accession: JC7104
A/Molecule type: mRNA
A/Residues: 1-155 <MUL>
A/Cross-references: GB:AF186094; NID:g6049804; PIDN:AAF02757.1; PID:g6049805
C/Genetics:
A/Gene: il1hy1
A/Map position: 2q14
C/Keywords: macrophage

```

Query Match          17.0%; Score 172.5; DB 2; Length 155;
Best Local Similarity 33.6%; Pred. No. 4.2e-09;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;

QY      34 FSIHQDHKVLVLDSGNLIAYDPKNYIRPEIFFALASSLSASAEG----- 80
      | : | | | | : | | | | : | | | | : | |
Db       9 FRMKDSALKVLYLHNNQL-----LAGGLHAGKVIKGEIISVVPNRWLDA 52

QY      81 --SPILLGVSKGEFCLYCKDKKGQSHPSLQLKKEKLMKL-AAQKESARRPFIFYRAQVGS 137
      | | : | | | | | | | | | | | | : | | | | : | | | | : |
Db       53 SLSPVILGVQGGSGQLSC--GVGO-EPTLTLEPVNIMELYGAKES--KSFTFYRRDMGL 107

QY      138 WNMLESAAHPGWFICTSCNCEPVGVTDKFEN 169
      : | | | : | | | | | : | | : | | | : | |
Db      108 TSFEESAAYPGWFICTYPEADQPVRLTQLPEN 139

```

RESULT 2
A44610
interleukin-1 receptor antagonist precursor - mouse
N/Alternate names: IL-1Ra
C/Species: Mus musculus (house mouse)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C/Accession: A44610; B40956; A49031; I56106; I52970
R/Matsushime, H.; Roussel, M.F.; Matsushima, K.; Hishinuma, A.; Sherr, C.J.
Blood 78, 616-623, 1991
A/Title: Cloning and expression of murine interleukin-1 receptor antagonist in macrophages
A/Reference number: A44610; MUID:91316273; PMID:1830498
A/Accession: A44610
A/Molecule type: mRNA
A/Residues: 1-178 <MAT>
A/Cross-references: GB:M64404; NID:g198296; PIDN:AAA39277.1; PID:g198297
R/Eisenberg, S.P.; Brewer, M.T.; Verdeber, E.; H  m  dal, P.; Brandhuber, B.J.; Thompson

```

Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991
A:/Title: Interleukin 1 receptor antagonist is a member of the Interleukin.1 gene family:
A:/Reference number: A40956; MUID:91271363; PMID:1828896
A:/Accession: B40956
A:/Molecule type: DNA
A:/Residues: 7-178 <EIS>
A:/Cross-references: GB:M63100; NID:g198389; PIDN:AAA39310.1; PID:g198390
R/Shuck, M.E.; Eessalu, T.E.; Tracey, D.E.; Bienkowski, M.J.
Eur. J. Immunol. 21, 2775-2780, 1991
A:/Title: Cloning, heterologous expression and characterization of murine interleukin 1 r
A:/Reference number: A49031; MUID:92037824; PMID:1834470
A:/Accession: A49031
A:/Molecule type: mRNA
A:/Residues: 23-178 <SHU>
A:/Cross-references: GB:S64082; NID:g238584; PIDN:AAB20265.1; PID:g238585
A:/Experimental source: peritoneal macrophages, TCR strain
A:/Note: sequence extracted from NCBI backbone (NCBIN:64082, NCBIF:64085)
R/Zahedi, K.; Seldin, M.F.; Rits, M.; Ezekowitz, R.B.; Whitehead, A.S.
J. Immunol. 146, 4228-4233, 1991
A:/Title: Mouse IL-1 receptor antagonist protein: Molecular characterization, gene mappin
A:/Reference number: I56106; MUID:91250712; PMID:1828262
A:/Accession: I56106
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: mRNA
A:/Residues: 1-178 <RES>
A:/Cross-references: GB:M74294; NID:g198387; PIDN:AAA39309.1; PID:g198388
R/Zahedi, K.A.; Uhlar, C.M.; Rits, M.; Prada, A.E.; Whitehead, A.S.
Cytokine 6, 1-9, 1994
A:/Title: The mouse interleukin 1 receptor antagonist protein: gene structure and regulat
A:/Reference number: I52970; MUID:94271931; PMID:8003626
A:/Accession: I52970
A:/Status: preliminary; translated from GB/EMBL/DBJ
A:/Molecule type: DNA
A:/Residues: 1-178 <RE2>
A:/Cross-references: GB:L32838; NID:g487864; PIDN:AAA20576.1; PID:g528978
C:/Genetics:
A:/Gene: IL-1rn
A:/Introns: 40/2; 70/1; 107/3
C:/Superfamily: Interleukin-1
C:/Keywords: cytokine receptor
F:/1-26/Domain: signal sequence #status predicted <SIG>
F:/27-178/Product: Interleukin-1 receptor antagonist #status predicted <MA2>

Query Match 15.6%; Score 159; DB 2; Length 178;
Best Local Similarity 32.7%; Pred. No. 9.6e-08;
Matches 48; Conservative 23; Mismatches 64; Indels 12; Gaps 7;

QY 34 FSIHQDHKVLVLDSGNLIAVPDKNYIR-PEIFFALASSLSASAEKSPILLGVSKGEF 92
| | | : | : | | | : | | | : | | | : | | | : |
Db 39 FRIMWTNQKTFYLRNNQLIA----GYLQGPNI--KLEEKIDMVPIDLHS-VFLGIHGKGL 91
| | | | | | | | | | | | | | | | | | | | | | | |
QY 93 CLYCDKDKGQSHPSLQLKKEKLMKLAQKESARRPFIYRAQVGSWMLESAHPGWFIC 152
| | | | | | | | | | | | | | | | | | | | | | | |
Db 92 CLSCAKSGDDI--KLQLEEVNITDLSKNKEDEKR-FTFIRSEKGPPTSFEAAACPGWFLC 148
| | | | | | | | | | | | | | | | | | | | | | | |
QY 153 TSCNCNEPVGVTDKFENRKHI-EFSFQ 178
| : | | | : | : | : | | |
Db 149 TTLLEADRPVSLFTNPPEPLIVTKFYFQ 175
| | | | | | | | | | | | | | | | | | | | | | | |

RESULT 3
A54377
Interleukin-1 receptor antagonist secreted form precursor - rabbit
C:/Species: Oryctolagus cuniculus (domestic rabbit)
C:/Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 16-Jul-1999
C:/Accession: A54377; I46729
R:/Cominelli, F.; Bortolami, M.; Pizarro, T.T.; Monsacchi, L.; Ferretti, M.; Brewer, M.T.
J. Biol. Chem. 269, 6962-6971, 1994
A:/Title: Rabbit Interleukin-1 receptor antagonist. Cloning, expression, functional chara
A:/Reference number: A54377; MUID:94165101; PMID:7509813
A:/Accession: A54377
A:/Molecule type: mRNA
A:/Residues: 1-177 <COM>

```

A;Cross-references: GB:S68977; NID:g545740; PIDN:AAB30093.1; PID:g545741
A;Experimental source: colon tissue
R;Note: sequence extracted from NCBI backbone (NCBIN:144168, NCBIP:144169)
R;Goto, F.; Goto, K.; Miyata, T.; Ohkawara, S.; Takao, T.; Morl, S.; Furukawa, S.; Ma
Immunology 77, 235-244, 1992
A;Title: Interleukin-1 recetor antagonist in inflammatory exudate cells of rabbits. P
A;Reference number: I46729; MUID:93052512; PMID:1427977
A;Accession: I46729
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-177 <GOT>
A;Cross-references: GB:D21832; NID:g425787; PIDN:BAA04860.1; PID:g452205
C;Superfamily: interleukin-1
C;Keywords: cytokine receptor; extracellular protein; glycoprotein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;109/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	14.9%;	Score 151.5;	DB 2;	Length 177;
Best Local Similarity	26.9%;	Pred. No. 5e-07;		
Matches 47;	Conservative 25;	Mismatches 50;	Indels 53;	Gaps 7;

```

QY      9  TETGKNSFEKKRLRGDPKVKNLNPKKFSIHDDHKVLVLDGSLIA----- 53
      :| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     21  SETACRPSGKRPCR-----MQAFRIWDVNOQKTFYLRNNQLVAGYLOGPNAKLEERID 72

QY     54  -VPDKNYIRPEIFFALASSLSASAEKSPILLGVSKGEFCLYCDK--DKQSHPSLQLK 110
      || : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     73  VVP----LEPQLLF-----LGIQRGKLCLSGVKSGDKMKLH----LE 106

QY     111  KEKLMKLAOKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNCPNEPVGVTD 165
      : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db     107  AVNITDLGKNKEQDKR-FTFIRNSNGPFTTFESASCPGWFCLCTALEADQPVSLTN 160

```

RESULT 4
A39386
Interleukin-1 receptor antagonist, long intracellular splice form - human
N:Contains: interleukin-1 receptor antagonist, short intracellular splice form
C/Species: Homo sapiens (man)
C/Date: 28-Feb-1992 #sequence_revision 11-Apr-1997 #text_change 26-May-2000
C/Accession: I37893, A39386
R/Muzio, M.; Polentarutti, N.; Sironi, M.; Poli, G.; De Gioia, L.; Introna, M.; Manto
J. Exp. Med. 182, 623-628, 1995
A/Title: Cloning and characterization of a new isoform of the interleukin 1 receptor
A/Reference number: I37893; MUID:95355865; PMID:7629520
A/Accession: I37893
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-180 <RES>
A/Cross-references: EMBL:X84348; NID:g1008970; PIDN:CAA59087.1; PID:g1008971
R/Haskill, S.; Martin, G.; Van Le, L.; Morris, J.; Peace, A.; Bigler, C.F.; Jaffe, G.
Proc. Natl. Acad. Sci. U.S.A. 88, 3681-3685, 1991
A/Title: cDNA cloning of an intracellular form of the human interleukin 1 receptor an
A/Reference number: A39386; MUID:91219436; PMID:1827201
A/Accession: A39386
A/Molecule type: mRNA
A/Residues: 1-3,25-180 <HAS>
A/Cross-references: GB:M55646; NID:g186291; PIDN:AAA59138.1; PID:g186292
C/Comment: For an alternative splice form, see PIR:A30368
C/Genetics:
A/Gene: GDB:IL1RN
A/Cross-references: GDB:125897; OMIM:147679
A/Map position: 2q14.2-2q14.2
C/Superfamily: interleukin-1
C/Keywords: alternative splicing; cytokine receptor
F:1-180/Product: interleukin-1 receptor antagonist, long intracellular splice form #s
F:1-3,25-180/Product: interleukin-1 receptor antagonist, short intracellular splice f

Query Match	14.8%;	Score 150.5;	DB 2;	Length 180;
Best Local Similarity	28.0%;	Pred. No. 6.3e-07;		
Matches 46;	Conservative 29;	Mismatches 64;	Indels 25;	Gaps 8;
QY 5	DRRET-ETGKGNSEKKRLRGPKVKNINPKKFSIHDDQDHKVLVLDGSLIAVPDKNYIR-	61		

Db 22 DSKETICRPSGRKSSKM-----QAFRIWDVNQKTFYLRNNQLVA----GYLOG 65

QY 62 PEIFFALASSLSASAEKSGPILLGVSKGEFCLYCDKDGQSHPSLQLKKEKMLKLAQK 121

Db 66 PNV-NLEEKIDVPIEPHA-LFLGIGHGKMCLSCVKSDETR--LQLEAVNITDISENR 120

QY 122 ESARRPFIFYRAQVGSWMNLESAAHPGFICTSCNENPEVGYTD 165

Db 121 KQDKR-FAFIRSDSGPTTSFESACPGWFLCTAMEADQPVSLTN 163

RESULT 5

A30368

Interleukin-1 receptor antagonist secreted form precursor - human

C:Species: Homo sapiens (man)

C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-May-2000

C:Accession: A40956; I37894; A30368; S08160; S08159; A37822

R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thompson, Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene family:

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: A40956

A:Molecule type: DNA

A:Residues: 1-177 <EIS>

A:Cross-references: GB:M63099; NID:g186385; PIDN:AA41943.1; PID:g186386

R:Lennard, A.; Gorman, P.; Carrier, M.; Griffiths, S.; Scotney, H.; Sheer, D.; Solari, F Cytokine 4, 83-89, 1992

A:Title: Cloning and chromosome mapping of the human interleukin-1 receptor antagonist g

A:Reference number: I37894; MUID:92338323; PMID:1385987

A:Accession: I37894

A>Status: translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-177 <LEN>

A:Cross-references: EMBL:X64532; NID:g33798; PIDN:CAA45832.1; PID:g33799

R:Cartier, D.B.; Delbel Jr., M.R.; Dunn, C.J.; Tomich, C.S.C.; Laborde, A.L.; Slightom, J J.G.; Stieu, L.C.; Hardee, M.M.; Zurcher-Neely, H.A.; Reardon, I.M.; Heinrikson, R.L.; Tr Nature 344, 633-638, 1990

A:Title: Purification, cloning, expression and biological characterization of an interle

A:Reference number: A30368; MUID:90220867; PMID:2139180

A:Accession: A30368

A:Molecule type: mRNA

A:Residues: 1-177 <CAR>

A:Cross-references: GB:X53296; NID:g32578; PIDN:CAA37386.1; PID:g32579

A:Note: parts of this sequence, including the amino end of the mature protein, were conf

R:Eisenberg, S.P.; Evans, R.J.; Arend, W.P.; Verderber, E.; Brewer, M.T.; Hannum, C.H.; N Nature 343, 341-346, 1990

A:Title: Primary structure and functional expression from complementary DNA of a human I

A:Reference number: S08160; MUID:90136921; PMID:2137201

A:Accession: S08160

A>Status: not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-177 <E12>

A:Cross-references: GB:X52015; NID:g32576; PIDN:CAA36262.1; PID:g32577

R:Hannum, C.H.; Wilcox, C.J.; Arend, W.P.; Joslin, F.G.; Dripps, D.J.; Heimdal, P.L.; Ar Nature 343, 336-340, 1990

A:Title: Interleukin-1 receptor antagonist activity of a human interleukin-1 inhibitor.

A:Reference number: S08159; MUID:90136920; PMID:2137200

A:Accession: S08159

A:Molecule type: protein

A:Residues: 26-75;97-108;110-116;120-131;163-176 <HAN>

R:Blenkowski, M.J.; Bessalu, T.E.; Berger, A.E.; Truesdell, S.E.; Shelly, J.A.; Laborde, J. Biol. Chem. 265, 14505-14511, 1990

A:Title: Purification and characterization of interleukin 1 receptor level antagonist pr

A:Reference number: A37822; MUID:90354444; PMID:2143761

A:Accession: A37822

A:Molecule type: protein

A:Residues: 26-52;70-77;122-127;170-175 <BIE>

A:Experimental source: culture medium, PMA-stimulated THP-1 cells

C:Comment: For an alternative splice form, see PIR:A39386

C:Genetics:

A:Gene: GDB:IL1RN

A:Cross-references: GDB:125897; OMIM:147679

A;Map position: 2q14.2-2q14.2

A;Introns: 39/2; 69/1; 106/3

C:Superfamily: Interleukin-1

C;Keywords: alternative splicing; cytokine receptor; extracellular protein; glycopro

F;1-25/Domain: signal sequence #status predicted <SIG>

F;26-177/Product: interleukin-1 receptor antagonist #status experimental <MAT>

F;109/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 14.7%; Score 149.5; DB 2; Length 177;

Best Local Similarity 29.3%; Pred. No. 7.7e-07;

Matches 41; Conservative 28; Mismatches 60; Indels 11; Gaps 6;

QY 27 KNLNPKFSIHQDHKVLVLDGSLIAVPDPKNYIR-PEIFFALASSLSASAEKGPILL 85

Db 31 KSSKMQAFRIWDVNQKTFYLRNNQLVA---GYLOGPNV--NLEEKIDVPIEPHA-LFL 83

QY 86 GVSKEFCLYCDKDGQSHPSLQLKKEKMLKLAQKESARRPFIFYRAQVGSWMNLESAA 145

Db 84 GIHGKMCLSCVKSDETR--LQLEAVNITDISENRKQDKR-FAFIRSDSGPTTSFESAA 140

QY 146 HPGWFICTSCNENPEVGYTD 165

Db 141 CPGWFLCTAMEADQPVSLTN 160

RESULT 6

C40956

Interleukin-1 receptor antagonist precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 20-Mar-1992 #sequence_revision 20-Mar-1992 #text_change 16-Jul-1999

C:Accession: C40956

R:Eisenberg, S.P.; Brewer, M.T.; Verderber, E.; Heimdal, P.; Brandhuber, B.J.; Thomp Proc. Natl. Acad. Sci. U.S.A. 88, 5232-5236, 1991

A:Title: Interleukin 1 receptor antagonist is a member of the interleukin 1 gene fami

A:Reference number: A40956; MUID:91271363; PMID:1828896

A:Accession: C40956

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <EIS>

A:Cross-references: GB:M63101; NID:g204928; PIDN:AAA41434.1; PID:g204929

C:Superfamily: Interleukin-1

C;Keywords: cytokine receptor

Query Match 14.2%; Score 144.5; DB 2; Length 178;

Best Local Similarity 29.1%; Pred. No. 2.3e-06;

Matches 41; Conservative 20; Mismatches 53; Indels 27; Gaps 4;

QY 34 FSIHQDHKVLVLDGSLIA-----VPDKNYIRPEIFFALASSLSASAEKGPILL 84

Db 39 FRIMDTNOKTFYLRNNQLIAGYLQGPNTKLEKIDMVPIDF-----RNVF 83

QY 85 LGVSKGEFCLYCDKDGQSHPSLQLKKEKMLKLAQKESARRPFIFYRAQVGSWMNLESAA 144

Db 84 LGIHGKLCISCVKSGDDT--KLQLEAVNITDLNKNKEEDKR-FTFIRSETGPTTSFESL 140

QY 145 AHPGWFICTSCNENPEVGYTD 165

Db 141 ACPGWFLCTTLEADHPVSLTN 161

RESULT 7

S23010

Interleukin-1 beta precursor - sheep

N;Alternate names: hematopoietin-1; IL-1 beta

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 08-Jun-1994 #sequence_revision 22-Nov-1996 #text_change 15-Oct-1999

C:Accession: S23010; S43047; S13092; B61246

R;Seow, H.F.; Rothel, J.S.; David, M.J.; Wood, P.R. DNA Seq. 1, 423-426, 1991

A:Title: Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.

A:Reference number: S23010; MUID:92119335; PMID:1840515

A:Accession: S23010

A:Molecule type: mRNA

C;Date: 20-May-1994 #sequence_revision 01-Dec-1995 #text_change 16-Jul-1999
C;Accession: S38373
R;Vandenbroeck, K.; Fiten, P.; Beuken, E.; Martens, E.; Janssen, A.; van Damme, J.; Opde
Eur. J. Biochem. 217, 45-52, 1993
A;Title: Gene sequence, cDNA construction, expression in Escherichia coli and geneticall
A;Reference number: S38373; MUID:94039070; PMID:8223584
A;Accession: S38373
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-267 <VAN>
A;Cross-references: EMBL:X74568; NID:g407899; PIDN:CAA52660.1; PID:g407900
C;Genetics:
A;Introns: 16/2; 33/3; 99/1; 154/1; 197/3
C;Superfamily: Interleukin-1

Query Match 11.1%; Score 112.5; DB 2; Length 267;
Best Local Similarity 28.7%; Pred. No. 0.0042;
Matches 37; Conservative 24; Mismatches 59; Indels 9; Gaps 5;

OY 36 IHDQDHKVLVLD SGNLI AVPD--KNYIRPEIFALASSLSASA EKGSPILLGVSKGEFC 93
Db 124 LQDKDEKALVLAGPHE LKALHLLKGD LKREVFCMSFVQGDSDDK-IPVTLGIRKKNLY 182
OY 94 LYC-DKDKGSHPS LQ LKKEKLMKLAQKESARRPFI FYRAQVGSWMML ESAHPGWFI C 152
Db 183 LSCVMKD--DTP TLQL--EDVDPKSYPRKMEKRFV FYKTEIKNRVEFESALYPNWTIS 237
OY 153 TSCNCNEPV 161
Db 238 TSQA EOKPV 246

RESULT 11
I55969
Interleukin-1 beta precursor - mouse
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: I55969; A24719; S13029
R;Gray, P.W.; Glaister, D.; Chen, E.; Goeddel, D.V.; Pennica, D.
J. Immunol. 137, 3644-3648, 1986
A;Title: Two interleukin 1 genes in the mouse: Cloning and expression of the cDNA for mu
A;Reference number: I55969; MUID:87058957; PMID:3491144
A;Accession: I55969
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-269 <RES>
A;Cross-references: GB:M15131; NID:g198293; PIDN:AAA39276.1; PID:g309398
R;Telford, J.L.; Macchia, G.; Massone, A.; Carinci, V.; Palla, E.; Melli, M.
Nucleic Acids Res. 14, 9955-9963, 1986
A;Title: The murine interleukin 1-beta gene: structure and evolution.
A;Reference number: A24719; MUID:87117546; PMID:3492706
A;Accession: A24719
A;Molecule type: mRNA
A;Residues: 1-269 <TEL>
A;Cross-references: GB:X04964; NID:g52666; PIDN:CAA28637.1; PID:g52667
R;Daumy, G.O.; Wilder, C.L.; Merenda, J.M.; McCol, A.S.; Geoghegan, K.F.; Otterness, I.
FEBS Lett. 278, 98-102, 1991
A;Title: Reduction of biological activity of murine recombinant interleukin-1beta by sel
A;Reference number: S13029; MUID:91130610; PMID:1993481
A;Accession: S13029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 118-269 <DAV>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleavag
ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a
C;Genetics:
A;Gene: IL-1-beta
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;118-269/Product: interleukin-1 beta #status experimental <ILI>

Query Match 10.2%; Score 104; DB 1; Length 269;
Best Local Similarity 27.5%; Pred. No. 0.027;
Matches 41; Conservative 29; Mismatches 71; Indels 8; Gaps 6;
OY 34 FSIHDQHKVLVL-DSGNLI AVP-DKNYIRPEIFALASSLSASA EKGSPILLGVSKGE 91
Db 125 YRLRDEQOKSLV LSPYELKALHNGQINQVIFSMFVQGEPSNDK-IPVALGLKGN 183
OY 92 FCLYCDKDGQSHPS LQ LKKEKLMKLAQKESARRPFI FYRAQVGSWMML ESAHPGWFI 151
Db 184 LYLSCVMKDG T--PTLQL--ESVDPKQYPKKMEKRFVFNKIEVKSKEFEFESAEFPNWTI 239
OY 152 CTSCNCNEPVGVTDK FENRKHI EFSFQPV 180
Db 240 STSQAEHKPVFLGN- SGDIIDFTMESV 267

RESULT 12
ICHUIB
Interleukin-1 beta precursor [validated] - human
N;Alternate names: hematopoietin-1; IL-1 beta
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1986 #sequence_revision 15-May-1998 #text_change 15-Sep-2000
C;Accession: A25542; A29019; A94023; A93361; I51852; I65200; I38132; B27616; A01848;
R;Clark, B.D.; Collins, K.L.; Gandy, M.S.; Webb, A.C.; Auron, P.E.
Nucleic Acids Res. 14, 7897-7914, 1986
A;Title: Genomic sequence for human prointerleukin 1 beta: possible evolution from a
A;Reference number: A25542; MUID:87040762; PMID:3490654
A;Accession: A25542
A;Molecule type: DNA; mRNA
A;Residues: 1-5, 'K', 7-269 <CLA>
A;Cross-references: GB:X04500; NID:g33788
A;Note: the mRNA sequence had codon AAG for 6-Lys, the DNA sequence had GAG for 6-Gl
R;Bensl, G.; Raugel, G.; Palla, E.; Carinci, V.; Buonamassa, D.T.; Melli, M.
Gene 52, 95-101, 1987
A;Title: Human interleukin-1 beta gene.
A;Reference number: A29019; MUID:87248099; PMID:2954882
A;Accession: A29019
A;Molecule type: DNA
A;Residues: 1-269 <BEN>
A;Cross-references: GB:M15840; NID:g186281; PIDN:AAA74137.1; PID:g386816
R;Auron, P.E.; Webb, A.C.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.; Di
Proc. Natl. Acad. Sci. U.S.A. 81, 7907-7911, 1984
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: A94023; MUID:85088517; PMID:6083565
A;Accession: A94023
A;Molecule type: mRNA
A;Residues: 1-5, 'K', 7-269 <AUR>
A;Cross-references: GB:K02770; NID:g186268; PIDN:AAA36106.1; PID:g307043
R;March, C.J.; Mosley, B.; Larsen, A.; Cerretti, D.P.; Braedt, G.; Price, V.; Gillis,
Nature 315, 641-647, 1985
A;Title: Cloning, sequence and expression of two distinct human interleukin-1 complex
A;Reference number: A93361; MUID:85240547; PMID:2989698
A;Accession: A93361
A;Molecule type: mRNA
A;Residues: 1-269 <MAR>
A;Cross-references: GB:X02532; NID:g33789; PIDN:CAA26372.1; PID:g33790
A;Note: parts of this sequence, including the amino end of the mature form, were con
R;Webb, A.C.; Dinarello, C.A.; Rosenwasser, L.J.; Mucci, S.F.; Rich, A.; Wolff, S.M.,
Adv. Gene Technol. 22, 339-340, 1985
A;Title: Nucleotide sequence of human monocyte interleukin 1 precursor cDNA.
A;Reference number: I51852
A;Accession: I51852
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-5, 'K', 7-19, 'H', 21-110, 'Q', 112-176, 'A', 178-213, 'P', 215-269 <WEB>
A;Cross-references: GB:M54933; NID:g186287; PIDN:AAA59136.1; PID:g186288
R;Nishida, T.; Nishino, N.; Takano, M.; Kawai, K.; Bando, K.; Masui, Y.; Nakai, S.; I
Biochem. Biophys. Res. Commun. 143, 345-352, 1987
A;Title: cDNA cloning of IL-1 alpha and IL-1 beta from mRNA of U937 cell line.
A;Reference number: I52217; MUID:87156769; PMID:3493774
A;Accession: I65200
A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 1-269 <NIS>
A:Cross-references: GB:M15330; NID:g186283; PIDN:AAA59135.1; PID:g307045
R:Kotenko, S.V.; Bulenkov, M.T.; Veiko, V.P.; Epishin, S.M.; Lomakin, I.B.; Emel'yanov, I.I.; S.A.; Vinetskii, Y.P.
Dokl. Akad. Nauk SSSR 309, 1005-1008, 1989
A:Title: Cloning of the cDNA coding for human prointerleukin-1 alpha and prointerleukin-1 beta
A:Reference number: I38131; MUID:90249285; PMID:2635664
A:Accession: I38132
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-269 <KOT>
A:Cross-references: EMBL:X56087; NID:g35662; PIDN:CAA39567.1; PID:g35663
R:Zsebo, K.M.; Wypych, J.; Yuschenkoff, V.N.; Lu, H.; Hunt, P.; Dukes, P.P.; Langley, K. Blood 71, 962-968, 1988
A:Title: Effects of hematopoietin-1 and interleukin 1 activities on early hematopoietic A:Reference number: A90732; MUID:88184226; PMID:3281727
A:Accession: B27616
A:Molecule type: protein
A:Residues: 117-123, 'X', 125-126, 'X', 128 <ZSE>
R:Stevenson, F.T.; Bursten, S.L.; Fanton, C.; Locksley, R.M.; Lovett, D.H. Proc. Natl. Acad. Sci. U.S.A. 90, 7245-7249, 1993
A:Title: The 31-kDa precursor of interleukin 1alpha is myristoylated on specific lysines A:Reference number: A48293; MUID:93348250; PMID:8346241
A:Contents: annotation; myristylation of lysines
R:Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Killian, P.L.; Stern, A.S. Biochim. Biophys. Acta 1118, 25-35, 1991
A:Title: The role of arginine residues in interleukin 1 receptor binding.
A:Reference number: S19608; MUID:92110334; PMID:1837236
A:Contents: annotation; type 1 IL-1 receptor interaction site
A:Note: modification of Arg-120 by phenylglyoxal blocks receptor binding
R:Clore, G.M.; Gronenborn, A.M.
submitted to the Brookhaven Protein Data Bank, January 1991
A:Reference number: A50049; PDB:6ILB
A:Contents: annotation; conformation by (13)C- and (1)H-NMR, residues 117-269
R:Clore, G.M.; Wingfield, P.T.; Gronenborn, A.M. Biochemistry 30, 2315-2323, 1991
A:Title: High-resolution three-dimensional structure of interleukin 1beta in solution by A:Reference number: A44675; MUID:91159409; PMID:2001363
A:Contents: annotation; (1)H-NMR structural determination
R:Hazuda, D.J.; Strickler, J.; Simon, P.; Young, P.R. J. Biol. Chem. 266, 7081-7086, 1991
A:Title: Structure-function mapping of interleukin 1 precursors. Cleavage leads to a con A:Reference number: A39774; MUID:91201363; PMID:2016316
A:Contents: annotation
R:Finzel, B.C.; Watenpaugh, K.D.; Einspahr, H.M.
submitted to the Brookhaven Protein Data Bank, December 1989
A:Reference number: A50016; PDB:1ILB
A:Contents: annotation; X-ray crystallography, 2.0 angstroms, residues 119-269
R:Finzel, B.C.; Clancy, L.L.; Holland, D.R.; Muchmore, S.W.; Watenpaugh, K.D.; Einspahr, J. Mol. Biol. 209, 779-791, 1989
A:Title: Crystal structure of recombinant human interleukin-1beta at 2.0 angstrom resolu A:Reference number: A44666; MUID:90064532; PMID:2585509
A:Contents: annotation; X-ray crystallography, 2.0 angstroms
C:Comment: This protein lacks a conventional signal sequence for protein export. Cleavag ved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C:Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1a C:Genetics:
A:Gene: GDB:IL1B
A:Cross-references: GDB:120094; OMIM:147720
A:Map position: 2q13-2q21
A:Introns: 16/2; 33/3; 101/1; 156/1; 199/3
C:Superfamily: Interleukin-1
C:Keywords: cytokine; immunoregulation; inflammation; lipoprotein; lymphokine; macrophag F;117-269/Product: interleukin-1 beta #status experimental <IL1>
F;76/Binding site: myristate (Lys) (covalent) (partial) #status experimental
F;123/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 9.1%; Score 93; DB 1; Length 269;
Best Local Similarity 28.4%; Pred. No. 0.3;
Matches 40; Conservative 27; Mismatches 58; Indels 16; Gaps 8;

QY 26 VKNLNPKFSIHQDHKVLVLD SG--NLIAVPDKNY-IRPEIFALASSLSASAEKGSP 82

Db 119 VRSLN--CTLRDSQOKSLVM-SGPYELKALHLQGDMEQQVVFMSFVGEEESNDK-IP 173
QY 83 ILGVSKGEFLCYC--DKDKGSHPSLQLKKEKLMKLAQKESARPPFIYRAQVGSWNM 140
Db 174 VALGLEKENLYLSCVLKDKD---PTLQL--ESVDPKNYPKKMEKRFVENKIEINNKLE 227
QY 141 LESAAHPGWFTGSCNCPNPV 161
Db 228 FESAQFPNMYISTSQAEINMPV 248

RESULT 13
S34031
KTR3 protein - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR1445; protein YBR205w
C:Species: Saccharomyces cerevisiae
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: S34031; S46077; S34928
R:Jacquet, M.
submitted to the EMBL Data Library, January 1993
A:Reference number: S34022
A:Accession: S34031
A:Molecule type: DNA
A:Residues: 1-404 <JAC>
A:Cross-references: EMBL:Z21487; NID:g311665; PID:g311682
R:Busserau, F.; Demolis, N.; Jacquet, M.; Mallet, L.
submitted to the Protein Sequence Database, August 1994
A:Reference number: S46054
A:Accession: S46077
A:Molecule type: DNA
A:Residues: 1-404 <BUS>
A:Cross-references: EMBL:Z36074; NID:g536582; PID:g536583; MIPS:YBR205w
R:Busserau, F.; Mallet, L.; Gaillon, L.; Jacquet, M. Yeast 9, 797-806, 1993
A:Title: Yeast Sequencing Reports. A 12.8 kb segment, on the right arm of chromosome A:Reference number: S34925; MUID:93377417; PMID:8368014
A:Accession: S34928
A:Molecule type: DNA
A:Residues: 91-352 <B02>
A:Cross-references: EMBL:Z21487
C:Genetics:
A:Gene: SGD:KTR3
A:Cross-references: SGD:S0000409; MIPS:YBR205w
A:Map position: 2R
C:Keywords: transmembrane protein
F;22-45/Domain: transmembrane #status predicted <TMM>

Query Match 8.9%; Score 91; DB 2; Length 404;
Best Local Similarity 22.8%; Pred. No. 0.76;
Matches 36; Conservative 20; Mismatches 58; Indels 44; Gaps 55;

QY 35 SIHDQHKVLYLD SGNLIAVPDKNYIRPE-----IFFALASSLSASAEKSPIL 84
Db 2 SVH--HKKILMPKSALLIRKYQKIRSSFIGLIIVLSFLFMSGSRSPVPPIAQGTYSV 58
QY 85 LGVSKGEFLCYCDKDGSHPSLQLKKEKLMKLAQKESARPPFIYRAQVGSWNMLESA 144
Db 59 RVASKDYLMPTDKSQGVYHPVDDGKRKEKGMVTLARNS-----DLWNLVKSI 106
QY 145 AHPGWFTGSCNCPNPVGTDTKFKENKHIIEFSF--QP 179
Db 107 RH-----VEDRFNMYHYDWFVFLNDQP 128

RESULT 14
JC5646
Interleukin-1 beta - horse
C:Species: Equus caballus (domestic horse)
C>Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 20-Jun-2000
C:Accession: JC5646
R:Kato, H.; Youn, H.Y.; Ohashi, T.; Watari, T.; Goltsuka, R.; Tsujimoto, H.; Hasegawa Gene 177, 11-16, 1996

A;Title: Identification of an alternatively spliced transcript of equine interleukin-1 b
A;Reference number: JC5646; MUID:97080493; PMID:8921838
A;Accession: JC5646
A;Molecule type: mRNA
A;Residues: 1-214 <KAT>
A;Cross-references: DDBJ:D42165; NID:g2463549; PIDN:BAA22528.1; PID:g2463550
C;Comment: This protein mediates a variety of physiological response to infections and i
synthesis by hepatocytes, and stimulation of chondrocytes and synovial cells to produce
C;Superfamily: interleukin-1

Query Match	8.88;	Score 89.5;	DB 2;	Length 214;
Best Local Similarity	27.38;	Pred. No. 0.49;		
Matches	27;	Conservative 17;	Mismatches 50;	Indels 5;
			Gaps	3;

```

QY      63 EIFFALASSLSASAEKSPILLGVSGEEFCLYCDKDKGSHPSLQLKKEKIMLAQKE 122
      ,  | : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db     100 EVVEFCMSFVGEEETDK-IPVALGLKEKNLYLSCGMKDGK--PTQL--ETVDPNTPYPR 154

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QY      123 SARPFIFRYAÖVGSWNMLESAHPGWFICTSCNCNEPV 161
      :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      155 KMEKRFVENKMEIKGVFEFESAMPNNWYISTSOAEKSPV 193
```

RESULT. 15

Interleukin-1 beta precursor - rabbit
N;Alternate names: hematopoietin-1; IL-1 beta; lymphocyte proliferation potentiating factor
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 25-May-1989 #sequence_revision 22-Nov-1996 #text_change 22-Jun-1999
C;Accession: A27714; A30584; J00082; A32166
R;Mori, S.; Goto, F.; Goto, K.; Ohkawara, S.; Maeda, S.; Shimada, K.; Yoshinaga, M.
Biochem. Biophys. Res. Commun. 150, 1237-1243, 1988
A;Title: Cloning and sequence analysis of a cDNA for lymphocyte proliferation potentiating factor
A;Reference number: A27714; MUID:88134238; PMID:2449207
A;Accession: A27714
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-268 <MOR>
R;Cannon, J.G.; Clark, B.D.; Wingfield, P.; Schmeissner, U.; Losberger, C.; Dinarello, C.
J. Immunol. 142, 2299-2306, 1989
A;Title: Rabbit IL-1. Cloning, expression, biologic properties, and transcription during infection
A;Reference number: A30584; MUID:89176242; PMID:2784458
A;Accession: A30584
A;Molecule type: mRNA
A;Residues: 1-268 <CAN>
A;Cross-references: GB:M26295; NID:g516632; PIDN:AAA31373.1; PID:g516633
R;Young, P.R.; Sylvester, D.
Protein Eng. 2, 545-551, 1989
A;Title: Cloning of rabbit interleukin-1 beta: differential evolution of IL-1 alpha and IL-1 beta
A;Reference number: A94230; MUID:89315718; PMID:2787507
A;Accession: J00082
A;Molecule type: mRNA
A;Residues: 1-268 <YOU>
C;Comment: This protein lacks a conventional signal sequence for protein export. Cleaved form of interleukin-1beta, unlike interleukin 1-alpha, is inactive.
C;Comment: Interleukin-1beta precursor is less heavily myristoylated than interleukin-1alpha
C;Superfamily: interleukin-1
C;Keywords: cytokine; immunoregulation; inflammation; lymphokine; macrophage; mitogen
F;117-268/Product: interleukin-1 beta #status predicted <ILB>

Query Match	8.8%;	Score 89;	DB 1;	Length 268;
Best Local Similarity	25.9%;	Pred. No. 0.72;		
Matches 36;	Conservative 24;	Mismatches 61;	Indels 18;	Gaps 5;

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QY      42 KVLVLDGSLIAPDKNYIRPEIFFALASSLSASAEKGPILLYSGKEFCLYC--DKD 99  
        | | | : | |          :: | : : | | : | : | | | |  
Db     142 KALHINAENL-----NQOVFSMSFVGEEESNDK-IPVALGIKGNLYLSCVMKD 191
```

```
QY 100 KGQSHPSIQLKKEKLMKLAQKESARPFIFYRAQVGSWMLESAAHPGWFICTSCNCNE 159
    | 1:111 | : : :1:1 : : 111 | 1:111
Db 192 K---PTIOL--ESVDPNRYPKKKMEKREVENKIEIKDLFEFSAQFPNNYISTQTEYM 245
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QY 160 PVGVTDKFNKRHIEFSQ 178

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Db      246 PVFLGNNSSGGQDLIDFSME 264
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Search completed: May 3, 2003, 18:38:52
Job time : 76 secs
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GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 3, 2003, 06:31:37 ; Search time 65 Seconds
(Without alignments)
122.515 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRRETETKGNSEFKR.....IEFSQPVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	159	15.6	178	IL1X_MOUSE	P25085 mus musculu
2	152	14.9	174	IL1X_BOVIN	O77482 bos taurus
3	151.5	14.9	177	IL1X_RABIT	P26890 oryctolagus
4	149.5	14.7	177	IL1X_HUMAN	P18510 homo sapien
5	146.5	14.4	177	IL1X_PIG	Q29056 sus scrofa
6	144.5	14.2	178	IL1X_RAT	P25086 rattus norv
7	137.5	13.5	177	IL1X_HORSE	O18999 equus cabal
8	127.5	12.5	266	IL1B_SHEEP	P21621 ovis aries
9	119.5	11.8	267	IL1B_PIG	P26889 sus scrofa
10	112.5	11.1	266	IL1B_BOVIN	P09428 bos taurus
11	109.5	10.8	266	IL1B_CAPHI	P79162 capra hircu
12	107	10.5	268	IL1B_RAT	Q63264 rattus norv
13	105	10.3	266	IL1B_CEREL	P51745 cervus elap
14	104	10.2	269	IL1B_MOUSE	P10749 mus musculu
15	101	9.9	269	IL1B_TRIUV	Q9xs77 trichosurus
16	98.5	9.7	266	IL1B_CAVPO	Q9wvq1 cavia porce
17	93	9.1	269	IL1B_HUMAN	P01584 homo sapien
18	92.5	9.1	268	IL1B_HORSE	Q28386 equus cabal
19	91	8.9	404	KTR3_YEAST	P38130 saccharomyc
20	89.5	8.8	267	IL1B_FELCA	P41687 felis silve
21	89	8.8	268	IL1B_RABIT	P14628 oryctolagus
22	88.5	8.7	269	IL1B_CERTO	P46648 cercocebus
23	88.5	8.7	269	IL1B_MACMU	P48090 macaca mula
24	88	8.7	473	MDM2_XENLA	P56273 xenopus lae
25	86	8.5	269	IL1B_MACNE	P51493 macaca neme
26	84	8.3	270	IL1A_MOUSE	P01582 mus musculu
27	84	8.3	2314	AKA6_RAT	Q9wvc7 rattus norv
28	83.5	8.2	268	IL1B_MACFA	P79182 macaca fasc
29	77	7.6	2209	Y166_HUMAN	P50748 homo sapien
30	76	7.5	425	YJ94_CAEEL	Q22236 caenorhabdl
31	76	7.5	448	EXG1_YEAST	P23776 saccharomyc
32	76	7.5	501	C72N_ARATH	Q9ltm0 arabidopsys
33	74.5	7.3	256	YKJ9_YEAST	P34247 saccharomyc

34	73.5	7.2	268	1	IL1A_CAPHI	P79161 capra hircu
35	73.5	7.2	418	1	NER3_MOUSE	Q9jmh7 mus musculu
36	73	7.2	390	1	TGF1_PIG	P07200 sus scrofa
37	72	7.1	271	1	IL1A_MACFA	P79340 macaca fasc
38	72	7.1	401	1	MYC2_CYPCA	Q90342 cyprinus ca
39	72	7.1	2319	1	AKA6_HUMAN	Q13023 homo sapien
40	71.5	7.0	270	1	IL1A_RAT	P16598 rattus norv
41	71.5	7.0	340	1	MMOC_METTR	Q53563 methylosinu
42	71.5	7.0	1282	1	TP2M_DICDI	P90520 dictyosteli
43	71.5	7.0	1469	1	DP27_CAEEL	P48996 caenorhabdl
44	71	7.0	334	1	MTN3_NEILA	P24582 neisseria 1
45	70.5	6.9	227	1	SYT_PSESY	P52833 pseudomonas

ALIGNMENTS

RESULT 1	ID	IL1X_MOUSE	STANDARD;	PRT;	178 AA.
AC	P25085; 070207;				
DT	01-MAY-1992 (Rel. 22, Created)				
DT	01-MAY-1992 (Rel. 22, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)				
DE	(IRAP).				
GN	IL1RN OR IL-1RA.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=91250712; PubMed=1828262;				
RA	Zahedi K., Seldin M.F., Rits M., Ezekowitz R.A., Whitehead A.S.;				
RT	"Mouse IL-1 receptor antagonist protein. Molecular characterization,				
RT	gene mapping, and expression of mRNA in vitro and in vivo."				
RL	J. Immunol. 146:4228-4233(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RX	MEDLINE=91316273; PubMed=1830498;				
RA	Matsushima H., Roussel M.F., Matsushima K., Hishinuma A., Sherr C.J.;				
RT	"Cloning and expression of murine interleukin-1 receptor antagonist				
RT	in macrophages stimulated by colony-stimulating factor 1."				
RL	Blood 78:616-623(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A. (ISOFORM 1).				
RC	STRAIN=Swiss;				
RX	MEDLINE=94271931; PubMed=8003626;				
RA	Zahedi K.A., Uhlar C.M., Rits M., Prada A.E., Whitehead A.S.;				
RT	"The mouse interleukin 1 receptor antagonist protein: gene structure				
RT	and regulation in vitro."				
RL	Cytokine 6:1-9(1994).				
RN	[4]				
RP	SEQUENCE FROM N.A. (ISOFORM 2).				
RC	STRAIN=FVB X DBA/1 LACJ;				
RX	MEDLINE=98209757; PubMed=9550387;				
RA	Gabay C., Porter B., Fantuzzi G., Arend W.P.;				
RT	"Mouse IL-1 receptor antagonist isoforms: complementary DNA cloning				
RT	and protein expression of intracellular isoform and tissue				
RT	distribution of secreted and intracellular IL-1 receptor antagonist in				
RT	vivo."				
RL	J. Immunol. 159:5905-5913(1997).				
RN	[5]				
RP	SEQUENCE OF 7-178 FROM N.A.				
RX	MEDLINE=91271363; PubMed=1828896;				
RA	Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,				
RA	Brandhuber B.J., Thompson R.C.;				
RT	"Interleukin 1 receptor antagonist is a member of the interleukin 1				
RT	gene family: evolution of a cytokine control mechanism."				
RL	Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).				
RP	[6]				
	SEQUENCE OF 23-178 FROM N.A.				

```

RX MEDLINE=92037824; PubMed=1834470;
RA Shuck M.E., Eessalu T.E., Tracey D.E., Bienkowski M.J.;
RT "Cloning, heterologous expression and characterization of murine
RT Interleukin 1 receptor antagonist protein.";
RL Eur. J. Immunol. 21:2775-2780(1991).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC (ISOFORM 2).
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC produced by alternative splicing.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M74294; AAA39309.1; -
DR EMBL; M64404; AAA39277.1; -
DR EMBL; L32838; AAA20576.1; -
DR EMBL; AF001795; AAC15251.1; -
DR EMBL; M57525; AAA39278.1; -
DR EMBL; M63100; AAA39310.1; -
DR EMBL; S64082; AAB20265.1; -
DR PIR; B40956; B40956.
DR PIR; A44610; A44610.
DR HSSP; P18510; 1IRA.
DR MGD; MGI:96547; Il1rn.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 2.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 26 BY SIMILARITY.
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 1 21 MEICWGPYSHLSILLILLFH -> MA (IN ISOFORM
FT 2).
SQ SEQUENCE 178 AA; 20274 MW; 84AA002A3119C024 CRC64;
Query Match 15.6%; Score 159; DB 1; Length 178;
Best Local Similarity 32.7%; Pred. No. 2.7e-08;
Matches 48; Conservative 23; Mismatches 64; Indels 12; Gaps 7;
QY 34 FSIHQDHKVLVDSGNLIAPVDKNYIR-PEIFPALASSISASAEKGSPIILGYSKGEF 92
| | | : | | : | | | | : | | | : | | : |
DB 39 FRIMWTNOKTFYLRNQOLIA---GYLGPNI--KLEEKIDMVPIDLHS-VFLGIHGKXL 91
QY 93 CLYCDKDKGQSHPSIQLKKEKIMKLAQAQESARSPFIYRAQVGSWMNLESAHPGWFIC 152
| | | | | | | : | : | : | : | : | : | : |
DB 92 CLSCAKSGDDI--KLQLEVENITDLSKNKEEDKR-FTFIRSEKGPPTSFEASACPWFCLC 148
QY 153 TSCNCNEPVGVTDKFENRKHI-EFSFQ 178
| : | : | : | : | : | : | : | : |
DB 149 TTLEADRPVSLTNTPEEPPLIVTKFYFQ 175
RESULT 2
IL1X_BOVIN
ID IL1X_BOVIN STANDARD; PRT; 174 AA.
AC 077482;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).

```

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GN  IL1RN.
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC  Bovidae; Bovinae; Bos.
OX  NCBI_TaxID=9913;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=98305607; PubMed=9643454;
RA  Kirisawa R., Fukuda T., Yamataka H., Hagiwara K., Goto M., Obata Y.,
RA  Yoshino T., Iwai H.;
RT  "Enzymatic amplification and expression of bovine Interleukin-1
RL  receptor antagonist cDNA.";
CC  Vet. Immunol. Immunopathol. 62:197-208(1998).
CC  -|- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC  RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC  -|- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AB005148; BAA31854.1; -.
DR  HSSP; P18510; IL1R.
DR  InterPro; IPR000975; Interleukin_1.
DR  Pfam; PF00340; IL1; 1.
DR  ProDom; PD002536; Interleukin_1; 1.
DR  SMART; SM00125; IL1; 1.
DR  PROSITE; PS00253; INTERLEUKIN_1; 1.
KW  Glycoprotein; Signal.
FT  SIGNAL 1 23 BY SIMILARITY.
FT  CHAIN 24 174 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT  PROTEIN.
FT  DISULFID 89 139 BY SIMILARITY.
FT  CARBOHYD 107 107 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE 174 AA; 19926 MW; 1E56E7F224FF851F CRC64;

Query Match 14.9%; Score 152; DB 1; Length 174;
Best Local Similarity 29.6%; Pred. No. 1.2e-07;
Matches 48; Conservative 18; Mismatches 54; Indels 42; Gaps 6;

QY 34 FSIHQDQHKVLVLDSGNLIA-----VPPKNVIRPEIFALASSLSASA 77
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 36 FRIMDVNQKIFYLRNNQLVAGYLQGPNTKLEEKIDVVP-----IEPHTMF----- 80

QY 78 EKGSPILLGVSKGEFLCYCDKDGQSHPSLOLKKREKLMKLAQKESARRPFIFYRAQVGS 137
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 81 -----LGIHGKILCLACVKSQDEI--KLKLEAVNITDLNQNRQDKR-FAFIRFDNGP 130

QY 138 WNMLESAAHPGWFICTSCGNCNEPVGVD-KFENRKHIIEFSQ 178
   1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
Db 131 TTSFESAACPFWFLCTSLIADQPVGLTNMPTEALKVTKRYFQ 172

RESULT 3
IL1X_RABIT
ID IL1X_RABIT STANDARD; PRT; 177 AA.
AC P26890;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]

```


RP SEQUENCE FROM N.A.
RX MEDLINE=94165101; PubMed=7509813;
RA Cominelli F., Bortolami M., Pizarro T.T., Monsacchi L., Ferretti M.,
RA Brewer M.T., Eisenberg S.P., Ng R.K.;
RT "Rabbit interleukin-1 receptor antagonist. Cloning, expression,
RT functional characterization, and regulation during intestinal
RT inflammation.";
RL J. Biol. Chem. 269:6962-6971(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Hamada H., Mulligan R.C.;
RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93052512; PubMed=1427977;
RA Goto F., Goto K., Miyata T., Ohkawara S., Takao T., Mori S.,
RA Furukawa S., Maeda T., Iwanaga S., Shimonishi Y., Yoshinaga M.;
RT "Interleukin-1 receptor antagonist in inflammatory exudate cells of
RT rabbits. Production, purification and determination of primary
RT structure.";
RL Immunology 77:235-244(1992).
RN [1]
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC
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CC
DR EMBL: S68977; AAB30093.1; -
DR EMBL: M57526; AAA31374.1; -
DR EMBL: D21832; BAA04860.1; -
DR PIR: A54377; A54377.
DR HSSP: P18510; 1ILR.
DR InterPro: IPR000975; Interleukin_1.
DR Pfam: PF00340; IL1; 1.
DR ProDom: PD002536; Interleukin_1; 1.
DR SMART: SM00125; IL1; 1.
DR PROSITE: PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20214 MW; F5BC087F097FEEAF CRC64;

Query Match 14.9%; Score 151.5; DB 1; Length 177;
Best Local Similarity 26.9%; Pred. No. 1.4e-07;
Matches 47; Conservative 25; Mismatches 50; Indels 53; Gaps 7;

OY 9 TETGKNSFKRLRGPKVKNLNPKKFSIHQDHLVLDGSLIA----- 53
DB 21 SETACRPSGKRPCR-----MQAFRIWDVNQKTFYLRNNQLVAGYLOGPNAKLEERID 72
OY 54 -VPDKNYIRPEIFALASSLSASAEGSPILGVSKGEFLCYDK--DKGQSHPSLQTK 110
DB 73 VVP---LEPQLLF-----LGIQGKICLSCVKSQDKMKLH---LE 106
OY 111 KEKLMKLAQKESARRPFIFYRAQVGSWNMLESAAHPGWFICTSCNENPVGVTD 165
DB 107 AVNTIDLGKNEQDKR-FTFIRSNSGPFTTFESASCPGWFICTALEADQPVSLTN 160

RESULT 4
IL1X_HUMAN
ID IL1X_HUMAN STANDARD; PRT; 177 AA.
AC P18510; O14628; Q9UPC0;
DT 01-NOV-1990 (Rel. 16, Created)

DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (ICIL-
DE 1RA) (IRAP) (IL-1RN).
GN IL1RN OR IL1RA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90220867; PubMed=2139180;
RA Carter D.B., Deibel M.R. Jr., Dunn C.J., Tomich C.S.C., Laborde A.L.,
RA Slightom J.L., Berger A.E., Bienkowski M.J., Sun F.F., McEwan R.N.,
RA Harris P.K.W., Yem A.W., Waszak G.A., Chosay J.G., Siew L.C.,
RA Hardee M.M., Zurcher-Neely H.A., Reardon I.M., Heinrichson R.L.,
RA Truesdell S.E., Shelly J.A., Bessalu T.E., Taylor B.M., Tracey D.E.;
RT "Purification, cloning, expression and biological characterization of
RT an interleukin-1 receptor antagonist protein.";
RL Nature 344:633-638(1990).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=90136921; PubMed=2137201;
RA Eisenberg S.P., Evans R.J., Arend W.P., Verderber E., Brewer M.T.,
RA Hannum C.H., Thompson R.C.;
RT "Primary structure and functional expression from complementary DNA
RT of a human interleukin-1 receptor antagonist.";
RL Nature 343:341-346(1990).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heimdal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin 1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=92338323; PubMed=1385987;
RA Lennard A., Gorman P., Carrier M., Griffiths S., Scotney H.,
RA Sheer D., Solari R.;
RT "Cloning and chromosome mapping of the human interleukin-1 receptor
RT antagonist gene.";
RL Cytokine 4:83-89(1992).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=97146044; PubMed=8992991;
RA Jenkins J.K., Drong R.F., Shuck M.E., Bienkowski M.J., Slightom J.L.,
RA Arend W.P., Smith M.F. Jr.;
RT "Intracellular IL-1 receptor antagonist promoter: cell type-specific
RT and inducible regulatory regions.";
RL J. Immunol. 158:748-755(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=91219436; PubMed=1827201;
RA Haskill S., Martin G., van Le L., Morris J., Peace A., Bigler C.F.,
RA Jaffe G.J., Hammerberg C., Sporn S.A., Fong S., Arend W.P., Ralph P.;
RT "cDNA cloning of an intracellular form of the human interleukin 1
RT receptor antagonist associated with epithelium.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:3681-3685(1991).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RX MEDLINE=95355865; PubMed=7629520;
RA Muzio M., Polentarutti N., Sironi M., Poli G., De Gioia L.,
RA Introna M., Mantovani A., Colotta F.;
RT "Cloning and characterization of a new isoform of the interleukin 1
RT receptor antagonist.";
RL J. Exp. Med. 182:623-628(1995).
RN [8]
RP SEQUENCE OF 26-45.
RX MEDLINE=90136920; PubMed=2137200;
RA Hannum C.H., Wilcox C.J., Arend W.P., Joslin F.G., Dripps D.J.,
RA Heimdal P.L., Armes L.G., Sommer A., Eisenberg S.P., Thompson R.C.;

RT "interleukin-1 receptor antagonist activity of a human interleukin-1
RT inhibitor.";
RL Nature 343:336-340(1990).
RN [9]
RP SEQUENCE OF 26-52.
RX MEDLINE=90354444; PubMed=2143761;
RA Blenkowski M.J., Eessalu T.E., Berger A.E., Truesdell S.E.,
RA Shelly J.A., Laborde A.L., Zurcher-Neely H.A., Reardon I.M.,
RA Heinrikson R.L., Chosay J.G., Tracey D.E.;
RT "Purification and characterization of interleukin 1 receptor level
RT antagonist proteins from THP-1 cells.";
RL J. Biol. Chem. 265:14505-14511(1990).
RN [10]
RP SEQUENCE OF 35-177 FROM N.A. (ISOFORM 4).
RX MEDLINE=98183404; PubMed=9514884;
RA Weisbach L., Tran K., Colquhoun S.A., Champlaud M.F., Towle C.A.;
RT "Detection of an interleukin-1 intracellular receptor antagonist mRNA
RT variant.";
RL Biochem. Biophys. Res. Commun. 244:91-95(1998).
RN [11]
RP STRUCTURE BY NMR.
RX MEDLINE=92297633; PubMed=1534997;
RA Stockman B.J., Scallill T.A., Roy M., Ulrich E.L., Strakalaitis N.A.,
RA Brunner D.P., Yem A.W., Deibel M.R. Jr.;
RT "Secondary structure and topology of interleukin-1 receptor
RT antagonist protein determined by heteronuclear three-dimensional NMR
RT spectroscopy.";
RL Biochemistry 31:5237-5244(1992).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=94320651; PubMed=8045306;
RA Stockman B.J., Scallill T.A., Strakalaitis N.A., Brunner D.P.,
RA Yem A.W., Deibel M.R. Jr.;
RT "Solution structure of human interleukin-1 receptor antagonist
RT protein.";
RL FEBS Lett. 349:79-83(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=94230368; PubMed=8175703;
RA Vigers G.P.A., Cafes P., Evans R.J., Thompson R.C., Eisenberg S.P.,
RA Brandhuber B.J.;
RT "X-ray structure of interleukin-1 receptor antagonist at 2.0-A
RT resolution.";
RL J. Biol. Chem. 269:12874-12879(1994).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=95172072; PubMed=7867645;
RA Schreuder H.A., Rondeau J.-M., Tardif C., Soffientini A., Sarubbi E.,
RA Akeson A., Bowlin T.L., Yanofsky S., Barrett R.W.;
RT "Refined crystal structure of the interleukin-1 receptor antagonist.
RT Presence of a disulfide link and a cis-proline.";
RL Eur. J. Biochem. 227:838-847(1995).
RN [15]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 32-177 IN COMPLEX WITH IL1R.
RX MEDLINE=97215904; PubMed=9062194;
RA Schreuder H., Tardif C., Trump-Kallmeyer S., Soffientini A.,
RA Sarubbi E., Akeson A., Bowlin T., Yanofsky S., Barrett R.W.;
RT "A new cytokine-receptor binding mode revealed by the crystal
RT structure of the IL-1 receptor with an antagonist.";
RL Nature 386:194-200(1997).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: SECRETED (ISOFORM 1) OR INTRACELLULAR
CC (ISOFORMS 2, 3 AND 4).
CC -1- ALTERNATIVE PRODUCTS: 4 isoforms; 1 (shown here), 2/ilc1-1ra,
CC 3/ilc1-1ra type II and 4; are produced by alternative splicing.
CC -1- TISSUE SPECIFICITY: THE INTRACELLULAR FORM OF IL-1RA IS
CC PREDOMINANTLY EXPRESSED IN EPITHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -1- DATABASE: NAME=R&D Systems' cytokine source book: IL1RN;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=205".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M55646; AAA59138.1; -
DR EMBL; M63099; AAB41943.1; -
DR EMBL; X52015; CAA36262.1; -
DR EMBL; X53296; CAA37386.1; -
DR EMBL; X64532; CAA45832.1; -
DR EMBL; U65590; AAB92268.1; -
DR EMBL; U65590; AAB92270.1; -
DR EMBL; X84348; CAA59087.1; -
DR EMBL; U65590; AAB92269.1; -
DR EMBL; AF043143; AAC39672.1; -
DR PIR; A30368; A30368.
DR PIR; A37822; A37822.
DR PIR; S08160; S08160.
DR PIR; S08159; S08159.
DR PIR; A40956; A40956.
DR PIR; A39386; A39386.
DR PDB; 1ITN; 30-APR-94.
DR PDB; 2IRT; 15-OCT-94.
DR PDB; 1IRP; 27-FEB-95.
DR PDB; 1ILR; 07-FEB-95.
DR PDB; 1ILT; 01-APR-95.
DR PDB; 1IRA; 17-JUN-98.
DR Aarhus/Ghent-2DPAGE; 7104; IEF.
DR Aarhus/Ghent-2DPAGE; 7105; IEF.
DR Genew; HGNC:6000; IL1RN.
DR MIM; 147679; -
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 3.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal; Alternative splicing; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 MEICRGLRSHLITLLEFLFHS -> MAL (IN
FT VARSPLIC 1 21 ISOFORM 2).
FT VARSPLIC 1 21 MEICRGLRSHLITLLEFLFHS -> MALADYEEGGGGGE
FT FT GEDNADSK (IN ISOFORM 3).
FT VARSPLIC 1 34 MISSING (IN ISOFORM 4).
SQ SEQUENCE 177 AA; 20055 MW; D1690776A7394057 CRC64;

Query Match 14.7%; Score 149.5; DB 1; Length 177;
Best Local Similarity 29.3%; Pred. No. 2.2e-07;
Matches 41; Conservative 28; Mismatches 60; Indels 11; Gaps 6;

QY 27 KNLNPKRESIHQDQDKVLVLDGSLIAVPDKNYIR-PEITFALASSLSASAEKGPILL 85
Db 31 KSKSKQAFRIMDVNOKTFYLRNQLVA---GYLQPNV--NLEEKIDVVPLEPBA-LFL 83
QY 86 GVSKEFCLYCDKDKGQSHPSIQLKKEKLMKLAQKESARRPFIFYRAQVGSWNMESSA 145
Db 84 GIHGKMKLSCVKSGDETR--IQLEAVNITDLSENRKDKR-FAFIRSDSGPTTSFESAA 140
QY 146 HPGWFICTSCNCPNPGVPTD 165
Db 141 CPGWFICTAMEADQPVSLTN 160

RESULT 5
IL1X_PIG
ID IL1X_PIG STANDARD; PRT; 177 AA.
AC Q29056;
DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IRAP1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Crossbred; TISSUE=Lung;
RA Yin J., Murtaugh M.P.;
RT "Characterization of IRAP in morphine treated pig."
RL Submitted (MAY-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; L38849; AAA99424.1; -.
DR HSSP; P18510; 1IRA.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Glycoprotein; Signal.
KW SIGNAL
FT 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 177 AA; 20093 MW; 2114DC6119A9D5F9 CRC64;

Query Match 14.4%; Score 146.5; DB 1; Length 177;
Best Local Similarity 28.4%; Pred. No. 4.3e-07;
Matches 42; Conservative 16; Mismatches 49; Indels 41; Gaps. 5;

QY 34 FSIHQDHKVLVLDGSLIA-----VDPKNYIRPEIFFALASSLSASASA 77
Db 38 FRWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVP---VEPHFVF----- 82

QY 78 EKGSPILGVSKGEFCLYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGS 137
Db 83 -----LGIHGKLCCLSCVKSGDEM-KLQLDVAVNITDLRKNSEQDKR-FTFIRSDSGP 132

QY 138 WNMLESAAHPGWFICTSCNCNEPVGVTD 165
Db 133 TTSFESAACPGWFLCTALEADQPVGLTN 160

RESULT 6
IL1X_RAT
ID IL1X_RAT STANDARD; PRT; 178 AA.
AC P25086;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, last sequence update)
DT 01-NOV-1995 (Rel. 32, last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL-1RA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91271363; PubMed=1828896;
RA Eisenberg S.P., Brewer M.T., Verderber E., Heindal P.,
RA Brandhuber B.J., Thompson R.C.;
RT "Interleukin-1 receptor antagonist is a member of the interleukin 1
RT gene family: evolution of a cytokine control mechanism."
RL Proc. Natl. Acad. Sci. U.S.A. 88:5232-5236(1991).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M63101; AAA41434.1; -.
DR PIR; C40956; C40956.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR Glycoprotein; Signal.
KW SIGNAL
FT 1 26 BY SIMILARITY.
FT CHAIN 27 178 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 92 142 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 178 AA; 20282 MW; F3A5754FB6C51B03 CRC64;

Query Match 14.2%; Score 144.5; DB 1; Length 178;
Best Local Similarity 29.1%; Pred. No. 6.7e-07;
Matches 41; Conservative 20; Mismatches 53; Indels 27; Gaps 4;

QY 34 FSIHQDHKVLVLDGSLIA-----VDPKNYIRPEIFFALASSLSASAEKSPIL 84
Db 39 FRWDVNQKTFYLRNNQLVAGYLQGPNTKLEEKIDVVIDF-----RNVF 83

QY 85 LGVSKGEFCLYCDKDGQSHPSLQKKKLMKLAQKESARRPFIFYRAQVGSNMLESA 144
Db 84 LGIHGKLCCLSCVKSGDDT-KLQLEEVNITDLNKNKEEDKR-FTFIRSETGPTTSFESL 140

QY 145 AHPGWFICTSCNCNEPVGVTD 165
Db 141 ACPGWFLCTTLEADHPVSLTN 161

RESULT 7
IL1X_HORSE
ID IL1X_HORSE STANDARD; PRT; 177 AA.
AC O18999; O77745;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, last sequence update)
DT 15-JUL-1999 (Rel. 38, last annotation update)
DE Interleukin-1 receptor antagonist protein precursor (IL-1RA) (IL-1RN)
DE (IRAP).
GN IL1RN OR IL1RA.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97366446; PubMed=9223227;
RA Kato H., Ohashi T., Matsushiro H., Watarai T., Goitsuka R.,
RA Tsujimoto H., Hasegawa A.;
RT "Molecular cloning and functional expression of equine interleukin-1

RT receptor antagonist.";
RL Vet. Immunol. Immunopathol. 56:221-231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98285942; PubMed=9622739;
RA Howard R.D., McIlwraith C.W., Trotter G.W., Nyborg J.K.;
RT "Cloning of equine interleukin-1 receptor antagonist and
RT determination of its full-length cDNA sequence.";
RL Am. J. Vet. Res. 59:712-716(1998).
CC -1- FUNCTION: IL-1RA INHIBITS THE ACTIVITY OF IL-1 BY BINDING TO ITS
CC RECEPTOR. IL-1RA HAS NO IL-1 LIKE ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
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CC -----
DR EMBL; D83714; BAA22529.1; -;
DR EMBL; U92482; AAC39257.1; -;
DR HSSP; P18510; IL1R.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Glycoprotein; Signal.
FT SIGNAL 1 25 BY SIMILARITY.
FT CHAIN 26 177 INTERLEUKIN-1 RECEPTOR ANTAGONIST
FT PROTEIN.
FT DISULFID 91 141 BY SIMILARITY.
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 19 19 F -> L (IN REF. 2).
SQ SEQUENCE 177 AA; 20459 MW; 1ABC377F1FCF80B CRC64;

Query Match 13.5%; Score 137.5; DB 1; Length 177;
Best Local Similarity 30.1%; Pred. No. 3.2e-06;
Matches 40; Conservative 22; Mismatches 62; Indels 9; Gaps 5;

QY 34 FSIHQDQHKVYLVDGSLIAVPDKNYIRPEIFFALASSLSASAEEKSPILLGVSGEFC 93
DB 38 FRIMDVNQKTFYMRNNQVA-----GYLQ-ESNTKLOEKIDVPIEPDA-LFLGLHGRKLC 91
QY 94 LYCDKDKGQSHPSLQKKKELMKLAQKESARRPFIFYRAQVGSWMLESAAHPGWFICT 153
DB 92 LACVKSQDEIR--FQLEAVNITDLSKNKEENK-FTFIRSNSSGPTTSFESAACPGWFLCT 148
QY 154 SCNCNEPVGVTDK 166
DB 149 AQEADRPVSLTNK 161

RESULT 8
IL1B_SHEEP
ID IL1B_SHEEP STANDARD; PRT; 266 AA.
AC P21621;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92119335; PubMed=1840515;
RA Seow H.F., Rothel J.S., David M.J., Wood P.R.;

RT "Nucleotide sequence of ovine macrophage interleukin-1 beta cDNA.";
RL DNA Seq. 1:423-426(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91088326; PubMed=2263490;
RA Fiskerstrand C., Sargan D.;
RT "Nucleotide sequence of ovine interleukin-1 beta.";
RL Nucleic Acids Res. 18:7165-7165(1990).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; X54796; CAA38566.1; -;
DR EMBL; X56972; CAA40293.1; -;
DR PIR; S13092; S13092.
DR PIR; S13810; S13810.
DR PIR; S23010; S23010.
DR HSSP; P01584; 511B.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113 INTERLEUKIN-1 BETA.
FT CHAIN 114 266
FT CONFLICT 14 14 Y -> C (IN REF. 2).
FT CONFLICT 55 55 Q -> K (IN REF. 2).
FT CONFLICT 64 64 V -> A (IN REF. 2).
FT CONFLICT 145 145 P -> L (IN REF. 2).
SQ SEQUENCE 266 AA; 30717 MW; BDED07B58224AB78 CRC64;

Query Match 12.5%; Score 127.5; DB 1; Length 266;
Best Local Similarity 29.5%; Pred. No. 4.8e-05;
Matches 39; Conservative 26; Mismatches 58; Indels 9; Gaps 6;

QY 33 KFSIHQDQHKVYLVDG---NLIAVPDKNYIRPEIFFALASSLSASAEEKSPILLGVSK 89
DB 120 KCKLQDRQKSLVLDSPVLKALHLPSEQMSR-EVVFQM-SFVQGEERDNKIPVALGIRD 177
QY 90 GEFCLYCDKDKGQSHPSLQKKKELMKLAQKESARRPFIFYRAQVGSWMLESAAHPGW 149
DB 178 KNLVLSQVK-KGDT-PTQL--EEVDPKVYPKRMMEKRFVYKTEIKNTVEFESVLPNW 233
QY 150 FICTSCNCNEPV 161
DB 234 YISTSQIEKPV 245

RESULT 9


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IL1B_PIG
ID IL1B_PIG STANDARD; PRT; 267 AA.
AC P26889;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314975; PubMed=8325511;
RA Huebner M.J., Lin G., Smith D.M., Murtaugh M.P., Molitor T.W.;
RT "Cloning, sequencing and regulation of an mRNA encoding porcine
RT Interleukin-1 beta.";
RL Gene 129:285-289(1993).
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M86725; AAA02584.1; -.
DR PIR; JN0724; JN0724.
DR HSSP; P01584; 1H1B.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR PRODOM; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
DR DR Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
KW Cytokine, Macrophage, Mitogen, Inflammatory response, Pyrogen.
FT PROPEP 1 114 BY SIMILARITY.
FT CHAIN 115 267 INTERLEUKIN-1 BETA.
FT SEQUENCE 267 AA; 30404 MW; 7F6B92B784D5086F CRC64;
SQ
Query Match 11.8%; Score 119.5; DB 1; Length 267;
Best Local Similarity 27.0%; Pred. No. 0.00028;
Matches 37; Conservative 27; Mismatches 64; Indels 9; Gaps 5;
OY 28 NLNPKFSIHDDHKVLVLDSCNLIAYPD--KNYIRPEIFRALASSLSASAEKGPILL 85
| : : :|:|:| | | : : : :|:|:| : : :|:|:|
Db 116 NVQSMECKLQDKDKHKSIVLAGPHMLKALHLTLGDLKREVVFCM-SFVQGDSDSNKIPVTL 174
| : : :|:|:| | | : : : :|:|:| : : :|:|:|
OY 86 GVSKEGFCLYC-DKDKGQSHSLQLKKEKLMKLAQKESARDFIYRAQVGSWMMLESA 144
| : | | | :|:|:| | : : :|:|:| : : :|:|:|
Db 175 GIKGKNLYLSCVMKD--NTPPLQL--EDIDPKRYPKRDMKEKREVFYKTEIKNRVEFESA 229
| :|:|:| | | :|:|:| | : : :|:|:| : : :|:|:|
OY 145 AHGWFICTSCNCNEPV 161
| :|:|:| | | :|:|:| | : : :|:|:| : : :|:|:|

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Db      230 LYPNWIYSTSQAEQKPV 246

RESULT 10
ID      IL1B_BOVIN          STANDARD;          PRT;          266 AA.
AC      P09428;
DT      01-MAR-1989 (Rel. 10, Created)
DT      01-MAR-1989 (Rel. 10, Last sequence update)
DT      30-MAY-2000 (Rel. 39, Last annotation update)
DE      Interleukin-1 beta precursor (IL-1 beta).
GN      IL1B.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89016591; PubMed=3262866;
RA      Leong S.R., Flagg G.M., Lawman M., Gray P.W.;
RT      "The nucleotide sequence for the cDNA of bovine interleukin-1 beta.";
RL      Nucleic Acids Res. 16:9054-9054(1988).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=88318652; PubMed=3261832;
RA      Maliszewski C.R., Baker P.E., Schoenborn M.A., Davis B.S., Cosman D.,
RT      Gillis S., Cerretti D.P.;
RT      "Cloning, sequence and expression of bovine interleukin 1 alpha and
RT      interleukin 1 beta complementary DNAs.";
RL      Mol. Immunol. 25:429-437(1988).
CC      -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC      THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC      MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC      IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC      IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC      THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC      -1- SUBUNIT: MONOMER.
CC      -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC      AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC      -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC      PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC      OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC      SECRETORY PROTEINS.
CC      -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; M35589; AAA30585.1; -
DR      EMBL; X12498; CAA31018.1; -
DR      EMBL; M37211; AAA30584.1; -
DR      PIR; J10010; ICB01B.
DR      PIR; S01380; S01380.
DR      HSSP; P01584; 1H1B.
DR      InterPro; IPR002348; IL1_HBGF.
DR      InterPro; IPR003502; IL1_Proprep.
DR      InterPro; IPR000975; Interleukin_1.
DR      Pfam; PF00340; IL1; 1.
DR      Pfam; PF02394; IL1_proprep; 1.
DR      PRINTS; PR00262; IL1HBGF.
DR      ProDom; PD002536; Interleukin_1; 1.
DR      SMART; SM00125; IL1; 1.
DR      PROSITE; PS00253; INTERLEUKIN_1; 1.
KW      Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT      PROPEP 1 113
FT      CHAIN 114 266 INTERLEUKIN-1 BETA.
FT      CONFLICT 252 252 A -> G (IN REF. 2).

```

SQ	SEQUENCE	266 AA;	30774 MW;	9DIEF8F5/5070586 CRC64;
	Query Match	11.1%;	Score 112.5;	DB 1; Length 266;
	Best Local Similarity	27.5%;	Pred. No. 0.0013;	
	Matches	36; Conservative	25; Mismatches	63; Indels 7; Gaps 5;
OY	33 KFSIHDDHKVVLVDSGNLIAVPD--KNYIRPEIFFAALSSLSASAEGSPILLGVSKG	90		
	: : : : : :			
Dd	120 KCKLQDRQKSLVLASPCVLKALHLLLSQEMNREVVFCM-SFVGGEERDNKIPIVALGIKKDK	178		
OY	91 EFCLYCDDKGQSHPSLOLKKEIKMLLAQKESARRPFIYRAQVGSWNMTESAHPGWFE	150		
	: : : : :			
Dd	179 NLYLSCVK-KGDT-PTQL--EEVDPKVYPKRNMKEKFVFYKTEIKNTVEEESVLYPNWY	234		
OY	151 ICTSCNCNEPV	161		
Dd	235 ISTSQIERPV	245		

```

RESULT 11
IL1B_CAPHI
ID IL1B_CAPHI STANDARD; PRT; 266 AA.
AC P79162;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Capra hircus (Goat).
OC Eumaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Hashimoto O., Mori Y., Tatsumi M.;
RT "Molecular cloning and expression of caprine IL-1alpha and
RT IL-1beta."
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
CC EMBL; D63351; BAA09675.1; -.
CC HSSP; P01584; 1HTB.
CC InterPro; IPR002348; IL1_HBGF.
CC InterPro; IPR003502; IL1_propep.
CC InterPro; IPR000975; Interleukin_1.
CC Pfam; PF00340; IL1; 1.
CC Pfam; PF02394; IL1_propep; 1.
CC PRINTS; PR00262; IL1HBGF.
CC PRODOM; PD002536; Interleukin_1; 1.
CC SMART; SM00125; IL1; 1.

```

DR	PROSITE; PS00253;	INTERLEUKIN_1; 1.
KW	Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.	
FT	PROPER	1 113 BY SIMILARITY.
FT	CHAIN	114 266 INTERLEUKIN-1 BETA.
SQ	SEQUENCE	266 AA; 30769 MW; 59F7B39BD1D4DDA5 CRC64;
Query Match		10.8%; Score 109.5; DB 1; Length 266;
Best Local Similarity		26.7%; Pred. No. 0.0026;
Matches	35; Conservative	25; Mismatches 64; Indels 7; Gaps 4;
QY	33 KFSIHDDHKVLVLDGSLIAVPD--KNYIRPEIFPALASSLSASAEKSGPILLGVSKG	90 : : : : : : : : :
Db	120 KCKLQDREQKSLVLDSPCVLAHLHLLSQEMSRREVFCM-SFVGGEERDNKIIPVALGIRDK	178
QY	91 EFCLYCDDKDQGSHPSLOLKEKKLMKLAQAOKESARRPFIFYRAQVGSWMNLESAAHPGWTF	150 : : : : : : : :
Db	179 N--LYLSWVKKGDTPTQL--EEVDPKVYPKRNMEEKREVEYKTEIKNTYEFESVLYPNWY	234
QY	151 ICTSCNCNEPV	161 :
Db	235 ISTSQIEEKPY	245

```

RESULT 12
ID IL1B_RAT STANDARD; PRT; 268 AA.
AC 063264;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Macrophage;
RA Reeser W., Freimark B.D.;
RL Submitted (Aug-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -1- SUBUNIT: MONOMER.
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M98820; AAA41426.1; -
DR HSSP; P10749; 2MIB.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD002536; Interleukin_1; 1.

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DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 116 BY SIMILARITY.
FT CHAIN 117 268 INTERLEUKIN-1 BETA.
SQ SEQUENCE 268 AA; 30644 MW; 109C19BEFF69C242D CRC64;

Query Match 10.5%; Score 107; DB 1; Length 268;
Best Local Similarity 27.9%; Pred. No. 0.0046;
Matches 41; Conservative 28; Mismatches 70; Indels 8; Gaps 6;

QY 36 IHDQDKVLVL-DSGNLIAPV-DKNYIRPEIFALASSLSASAEKSPILGVSKGEFC 93
Db 126 LRDEQCKLVLSDPELKLHLNGQNIQQVFSMSFVGETSNDK-IPVALGLKLNLY 184

QY 94 LYCDKDKGQSHPSLOLKEKIMKLAQKESARRPFIFYRAQVGSWMNLSAHPGWFICT 153
Db 185 LSCVMKDGTL--PTLQL--ESVDPKQYPKKKMEKRFVENKIEVKTKEFEESAQFPNWIYST 240

QY 154 SCNCNEPVGVTDKFEENRKHIEFSQPV 180
Db 241 SOAEHRPVFLGNS-NGRDIVDFTEMPV 266

RESULT 13

IL1B_CEREL
ID IL1B_CEREL STANDARD; PRT; 266 AA.
AC P51745;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervidae; Cervinae; Cervus.
OX NCBI_Taxid=9860;
RN [1]
RP SEQUENCE FROM N.A.
RA Lockhart E.A.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION AND PROLIFERATION, AND FIBROBLAST GROWTH FACTOR
CC ACTIVITY. IL-1 IS INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS
CC (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (By similarity).
CC -!- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -!- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS (By similarity).
CC -!- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; U20500; AAA62234.1; .
DR HSSP; P01584; 1H1B.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR Pfam; PF02394; IL1_propep; 1.

DR PRINTS; PR00262; IL1HBGF.
DR Prodom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.
FT PROPEP 1 113 BY SIMILARITY.
FT CHAIN 114 266 INTERLEUKIN-1 BETA.
SQ SEQUENCE 266 AA; 30629 MW; 4F40B4E6F0D9F060 CRC64;

Query Match 10.3%; Score 105; DB 1; Length 266;
Best Local Similarity 26.8%; Pred. No. 0.007;
Matches 37; Conservative 29; Mismatches 62; Indels 10; Gaps 6;

QY 26 VKNLNPKKFSIHDQDKVLVDSGNLIAPV--KNYIRPEIFALASSLSASAEKSGSPI 83
Db 116 VQSVNCK--LQDRQNSLVASPCVLKALHLLSQEMSRVVFECM-SFVQAEERDNKIPV 171

QY 84 LIGVSKGEFCLYCDKDKGQSHPSLOLKEKIMKLAQKESARRPFIFYRAQVGSWMNLS 143
Db 172 ALGIRDKNQYLSCVK-KGDT-PTLQL--EEVDPKVYPRKMKERFVFYKTEIKDVEFEES 227

QY 144 AAHPGWFICTSCNCNEPV 161
Db 228 VLYPNWYISTSHPEKPV 245

RESULT 14

IL1B_MOUSE
ID IL1B_MOUSE STANDARD; PRT; 269 AA.
AC P10749;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-1 beta precursor (IL-1 beta).
GN IL1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87058957; PubMed=3491144;
RA Gray P.W., Glaister D., Chen E., Goeddel D.V., Pennica D.;
RT "Two interleukin 1 genes in the mouse: cloning and expression of the
RT cDNA for murine interleukin 1 beta."
RL J. Immunol. 137:3644-3648(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87117546; PubMed=3492706;
RA Telford J.L., Macchia G., Massone A., Carinci V., Palla E., Melli M.;
RT "The murine interleukin 1 beta gene: structure and evolution."
RL Nucleic Acids Res. 14:9955-9963(1986).
RN [3]
RP SEQUENCE OF 118-139.
RX MEDLINE=88229074; PubMed=2967326;
RA Huang J.J., Newton R.C., Rutledge S.J., Horuk R., Matthew J.B.,
RA Covington M., Lin Y.;
RT "Characterization of murine IL-1 beta. Isolation, expression, and
RT purification."
RL J. Immunol. 140:3838-3843(1988).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=92222792; PubMed=1807351;
RA van Oostrum J., Priestle J.P., Grutter M.G., Schmitz A.;
RT "The structure of murine interleukin-1 beta at 2.8-A resolution."
RL J. Struct. Biol. 107:189-195(1991).
CC -!- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES
CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL
CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.
CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING
CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE
CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.
CC -!- SUBUNIT: MONOMER.

```
CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE
CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.
CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE
CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS
CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER
CC SECRETORY PROTEINS.
CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.
CC -----
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CC -----
DR EMBL; M15131; AAA39276.1; -
DR EMBL; X04964; CAA28637.1; -
DR PIR; A24719; A24719.
DR PIR; S13029; S13029.
DR PDB; 811B; 15-OCT-94.
DR PDB; 2M1B; 31-JAN-94.
DR MGD; MGI:96543; 111b.
DR InterPro; IPR002348; IL1_HBGF.
DR InterPro; IPR003502; IL1_propep.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1_1.
DR Pfam; PF02394; IL1_propep; 1.
DR PRINTS; PR00262; IL1HBGF.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen;
KW 3d-structure.
FT PROPEP 1 117
FT CHAIN 118 269 INTERLEUKIN-1 BETA.
FT STRAND 123 129
FT TURN 130 131
FT STRAND 134 137
FT TURN 140 141
FT STRAND 143 146
FT TURN 150 154
FT STRAND 159 163
FT TURN 170 171
FT STRAND 173 179
FT TURN 180 181
FT STRAND 184 191
FT TURN 192 193
FT STRAND 194 201
FT TURN 204 206
FT HELIX 214 216
FT STRAND 217 222
FT STRAND 227 231
FT TURN 235 236
FT STRAND 238 242
FT STRAND 247 248
FT STRAND 250 252
FT STRAND 258 259
FT STRAND 262 266
SQ SEQUENCE 269 AA; 30931 MW; 734FA17B02ED87EE CRC64;
```

Query Match 10.2%; Score 104; DB 1; Length 269;
Best Local Similarity 27.5%; Pred. No. 0.0089;
Matches 41; Conservative 29; Mismatches 71; Indels 8; Gaps 6;

```
OY 34 FSIHQDHKVLV-DSGNLIAVP-DKNYIRPEIFALASSLSASAEEKSPILLGVSKGE 91
Db 125 YRLRDEQOKSLVSDPYELKALHLNGQINNOQVIFSMFVQGEPSNDK-IPVALGLKGN 183
OY 92 FCLYCDKDKGQSHPSLQKKKELMKLAQKESARRPFIYRAQVGSWMMLSEAAHPGWFI 151
Db 184 LYLSCVMKDG-T-PTLQL--ESVDPKQYPPKKMKMEKREYFNKIEVKSKEVEFESAEFPNWI 239
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```
OY 152 CTSCNCEPVGVTDKFENRKHIESFQPV 180
Db 240 STSQAEHKPVFLGNN-SGQDIDFTMESV 267
```

RESULT 15

IL1B-TRIVU

ID IL1B-TRIVU STANDARD; PRT; 269 AA.

AC Q9XS77;

DT 15-JUN-2002 (Rel. 41, Created)

DT 15-JUN-2002 (Rel. 41, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Interleukin-1 beta precursor (IL-1 beta).

GN IL1B.

OS Trichosurus vulpecula (Brush-tailed possum).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Metatheria; Diprotodontia; Phalangeridae; Trichosurus.

OX NCBI_TaxID=9337;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99221044; PubMed-10206203;

RA Wedlock D.N., Goh L.P., Parlane N.A., Buddle B.M.;

RT "Molecular cloning and physiological effects of brushtail possum

RT Interleukin-1beta.";

RL Vet. Immunol. Immunopathol. 67:359-372(1999).

CC -1- FUNCTION: PRODUCED BY ACTIVATED MACROPHAGES, IL-1 STIMULATES

CC THYMOCYTE PROLIFERATION BY INDUCING IL-2 RELEASE, B-CELL

CC MATURATION & PROLIFERATION, & FIBROBLAST GROWTH FACTOR ACTIVITY.

CC IL-1 PROTEINS ARE INVOLVED IN THE INFLAMMATORY RESPONSE, BEING

CC IDENTIFIED AS ENDOGENOUS PYROGENS, AND ARE REPORTED TO STIMULATE

CC THE RELEASE OF PROSTAGLANDIN AND COLLAGENASE FROM SYNOVIAL CELLS.

CC -1- SUBUNIT: MONOMER.

CC -1- DOMAIN: THE SIMILARITY AMONG THE IL-1 PRECURSORS SUGGESTS THAT THE

CC AMINO ENDS OF THESE PROTEINS SERVE SOME AS YET UNDEFINED FUNCTION.

CC -1- MISCELLANEOUS: THE LACK OF A SPECIFIC HYDROPHOBIC SEGMENT IN THE

CC PRECURSOR SEQUENCE SUGGESTS THAT IL-1 IS RELEASED BY DAMAGED CELLS

CC OR IS SECRETED BY A MECHANISM DIFFERING FROM THAT USED FOR OTHER

CC SECRETORY PROTEINS.

CC -1- SIMILARITY: BELONGS TO THE IL-1 FAMILY.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AF071539; AAD21871.1; -

DR HSSP; P01584; 1H1B.

DR InterPro; IPR002348; IL1_HBGF.

DR InterPro; IPR003502; IL1_propep.

DR InterPro; IPR000975; Interleukin_1.

DR Pfam; PF00340; IL1_1.

DR Pfam; PF02394; IL1_propep; 1.

DR PRINTS; PR00262; IL1HBGF.

DR ProDom; PD002536; Interleukin_1; 1.

DR SMART; SM00125; IL1; 1.

DR PROSITE; PS00253; INTERLEUKIN_1; 1.

KW Cytokine; Macrophage; Mitogen; Inflammatory response; Pyrogen.

FT PROPEP 1 112 BY SIMILARITY.

FT CHAIN 113 269 INTERLEUKIN-1 BETA.

SQ SEQUENCE 269 AA; 31141 MW; 307A1FE3B627D6E7 CRC64;

Query Match 9.9%; Score 101; DB 1; Length 269;
Best Local Similarity 24.4%; Pred. No. 0.017;
Matches 39; Conservative 34; Mismatches 65; Indels 22; Gaps 8;

```
OY 4 CDRRETETKGNSEFKRLRGPKVKNLNPKKFSIHQDHKVLVLDGSLIAVPDKN--YIR 61
Db 111 CDYIESD-----SSFRL-----VSSQDCTTIQDINQKIALSKASELRALHLNGRIS 157
OY 62 PEIFFALASSLSASAEEKSPILLGVSKGEFCLYCDKDKGQSHPSLQKKKELMKLAQK 121
```



```
Db 158 QOVIFSMKYLGDIGSQK-THVVLICIKKNULYLSCVR-RGEK-PILOL-EQIANFPSIN 212
OY 122 ESARPFIFYRAQVGSWNMLESAHPCWFICTSCNCPV 161
Db 213 VEKR--FIENKVEINNTEFEESAEPNNTISTSQMDEQPV 250
```

Search completed: May 3, 2003, 18:35:42
Job time : 67 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 3, 2003, 18:21:35 ; Search time 89 Seconds
(without alignments)
444.506 Million cell updates/sec

Title: US-09-876-790-3
Perfect score: 1017
Sequence: 1 MSGCDRRETETKGKNSFKKR.....IEFSFQPVCKAEMSPSEVSD 192

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhlc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1017	100.0	192	4 Q9UHA6	Q9uha6 homo sapien
2	905	89.0	197	4 Q8TD05	Q8td05 homo sapien
3	895	88.0	218	4 Q9NZH6	Q9nzh6 homo sapien
4	895	88.0	218	4 Q9HBF3	Q9hbf3 homo sapien
5	704	69.2	178	4 Q9HBF2	Q9hbf2 homo sapien
6	688	67.6	157	4 Q8TD04	Q8td04 homo sapien
7	229	22.5	157	4 Q9UHA5	Q9uha5 homo sapien
8	225.5	22.2	169	4 Q9NZH8	Q9nzh8 homo sapien
9	209	20.6	158	4 Q9UHA7	Q9uha7 homo sapien
10	199	19.6	156	11 Q8R461	Q8r461 mus musculu
11	199	19.6	183	11 Q9D6Z6	Q9d6z6 mus musculu
12	189.5	18.6	155	11 Q9QYX1	Q9qyx1 mus musculu
13	189.5	18.6	156	11 Q9JIG2	Q9jig2 mus musculu
14	178.5	17.6	164	11 Q8R460	Q8r460 mus musculu
15	172.5	17.0	155	4 Q9UBH0	Q9ubh0 homo sapien
16	171.5	16.9	160	11 Q9JIA2	Q9jia2 mus musculu

17	165.5	16.3	152	11 Q8R459	Q8r459 mus musculu
18	156.5	15.4	152	4 Q8WWZ1	Q8wwz1 homo sapien
19	156	15.3	144	4 Q9BYX1	Q9byx1 homo sapien
20	155.5	15.3	152	4 Q969H5	Q969h5 homo sapien
21	151	14.8	172	13 Q9DDE2	Q9ddf2 cyprinus ca
22	150	14.7	177	6 Q9GMZ4	Q9gmz4 tursiops tr
23	149.5	14.7	159	4 Q96GD6	Q96gd6 homo sapien
24	149	14.7	176	6 Q9BEH0	Q9beh0 canis famli
25	149	14.7	267	13 Q73909	Q73909 gallus gall
26	140	13.8	272	13 Q9DDF3	Q9ddf3 cyprinus ca
27	139	13.7	176	6 Q9GKK2	Q9gkk2 canis famli
28	128	12.6	276	13 Q57398	Q57398 cyprinus ca
29	128	12.6	276	13 Q9PW18	Q9pw18 cyprinus ca
30	118.5	11.7	164	4 Q9NZH7	Q9nzh7 homo sapien
31	112.5	11.1	260	13 Q8UUC3	Q8uuc3 oncorhynch
32	112.5	11.1	260	13 Q9YGD3	Q9ygd3 oncorhynch
33	112.5	11.1	267	6 Q29082	Q29082 sus scrofa
34	111.5	11.0	247	13 Q8QGWO	Q8qgw0 paralicthn
35	107	10.5	72	6 Q77771	Q77771 equus cabal
36	107	10.5	254	13 Q9PT12	Q9pt12 oncorhynch
37	107	10.5	283	13 Q9PVZ5	Q9pvz5 xenopus lae
38	104	10.2	599	11 Q9IWP7	Q9iwp7 mus musculu
39	103	10.1	266	6 Q8WNR2	Q8wnr2 delphinapte
40	101	9.9	253	13 Q9OW32	Q9ow32 sparus aura
41	101	9.9	261	13 Q9OW84	Q9ow84 dicentrarch
42	99	9.7	266	6 Q9TTR1	Q9ttk1 tursiops tr
43	96	9.4	267	11 Q91ZL5	Q91z15 sigmodon hi
44	89.5	8.8	153	4 Q43645	Q43645 homo sapien
45	87	8.6	1064	4 Q9H7R7	Q9h7r7 homo sapien

ALIGNMENTS

RESULT 1
Q9UHA6 PRELIMINARY; PRT; 192 AA.
ID Q9UHA6
AC Q9UHA6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE FILI zeta.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Sims J.E.;
RL "Four New Members Expand the IL-1 Superfamily.";
J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201832; AAF25212.1; -.
DR HSSP; P18510; 1ILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
SQ SEQUENCE 192 AA; 21543 MW; 4AF584C81802F612 CRC64;

Query Match 100.0%; Score 1017; DB 4; Length 192;
Best Local Similarity 100.0%; Pred. No. 2.9e-96;
Matches 192; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MSGCDRRETETKGKNSFKRLRGPVKVKNLNPKKFSIHDDHKVLVLDGNNLJAVPDKNYI	60
DB	1	MSGCDRRETETKGKNSFKRLRGPVKVKNLNPKKFSIHDDHKVLVLDGNNLJAVPDKNYI	60
QY	61	RPEIFFALASSLSASAEKGSPIILGVSGEFCLYCDKDKGQSHPSLQKKKLMKLAQ	120
DB	61	RPEIFFALASSLSASAEKGSPIILGVSGEFCLYCDKDKGQSHPSLQKKKLMKLAQ	120

[illegible]

RESULT 2

ID	Q8TD05	PRELIMINARY;	PRT;	197 AA.
AC	Q8TD05;			
DT	01-JUN-2002	(TREMBLrel.	21,	Created)
DT	01-JUN-2002	(TREMBLrel.	21,	Last sequence update)
DT	01-JUN-2002	(TREMBLrel.	21,	Last annotation update)

05 Homo sapiens (Human).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
0X NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RA Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RT "Genomic Organization of the IL-1 Locus.";
RL Genomics 0:0-0(2002).
DR EMBL: AY071840; AAL67151.1; -
SQ SEQUENCE 197 AA; 21950 MW; 55BEA6540008B67A CRC64;

Query Match	89.08;	Score 905;	DB 4;	Length 197;
Best Local Similarity	99.48;	Pred. No. 9.1e-85;		
Matches 171; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy	21	LRGPKVKNLNPKKFSIHQDHKVLVLDGSLIAYBDKNYIRPEIFFALASSLSASAEGK	80
	+		
Db	26	LEGPVKNLNPKKFSIHQDHKVLVLDGSLIAYBDKNYIRPEIFFALASSLSASAEGK	85

```

0Y      81 SPILLGVSKHEFCLYCDKDKGQSHPSIQLKKEKLMKLAQKESARRPFIFYRAQVGSWNM 140
        |||||||
Db      86 SPILLGVSKHEFCLYCDKDKGQSHPSIQLKKEKLMKLAQKESARRPFIFYRAQVGSWNM 145

```

[illegible]

RESULT 3

Q9NZH6	PRELIMINARY;	PRT;	218 AA
ID	Q9NZH6		

DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE	Interleukin-1 homolog 4 (IL-1x protein) (Interleukin-1-related protein long isoform a).
DE	Homo sapiens (Human).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC	NCBI_TaxID=9606;
OX	

RP SEQUENCE FROM N.A.
RC TISSUE-FETAL LUNG, FETAL TESTIS, FETAL B-CELL, AND FETAL COLON;
RX MEDLINE=20209405; Pubmed=10744718;
RA Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,
RA Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,
RA Young P.R.?

RT "Identification and initial characterization of four novel members of
RT the interleukin-1 family.";
RT
RL J. Biol. Chem. 275:10308-10314(2000).

NO.	DATE	SEQUENCE FROM N.A.	TISSUE=COLON CARCINOMA;
RC			
RP			
RR			

RA Manoj P.P., Mantovani A., Muzio M.;
Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RA Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Yansura D.,
RA Lewis L., Eigenbrot C., Henzle W.J., Vandlen R., Filvaroff E.,
RT "IL-1H, an interleukin-1-related protein that binds IL-18 receptor/IL-
RT 1RFP.";

RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

DR	EMBL; AF200496; AAF69252.1; -
DR	EMBL; AF217368; AAG29344.1; -
DR	EMBL; AF251118; AAG14420.1; -
DR	HSSP; P18510; 11LR
DR	InterPro; IPR00975; Interleukin_1.
DR	Pfam; PF00340; 1L1. 1.
DR	ProDom; PD002536; Interleukin_1; 1.

```
DR SMART; SM00125; IL1; 1.  
SQ SEQUENCE 218 AA; 24126 MW; 96E089310D2CEA68 CRC64;
```

Query Match	88.0%;	Score 895;	DB 4;	Length 218;
Best Local Similarity	100.0%;	Pred. No. 1.1e-83;		
Matches 169;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      24 PKVKNLNPKKSIHQDHKVLVLDGSLTAVPDKNYIRPEIFPALASSLSASAEGSP I 83  
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db     50 PKVKNLNPKKSIHQDHKVLVLDGSLTAVPDKNYIRPEIFPALASSLSASAEGSP I 109
```

QY	84	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKIMKLAQAQESARPEIFYRAQVGSWMNLES	1433
Db	110	LLGVSKGEFCLYCDKDKGQSHPSLQLKKEKIMKLAQAQESARPEIFYRAQVGSWMNLES	1699

QY	144	AAHPGWFICTSCNCPVGVTDKFENRKHTIEFSQPVCKAEMSPSEYSD	1922
Db	170	AAHPGWFICTSCNCPVGVTDKFENRKHTIEFSQPVCKAEMSPSEYSD	2188

RESULT 4

Q9HBF3
ID Q9HBF3 PRELIMINARY; PRT; 218 AA.

DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE	Interleukin-1-related protein long isoform (Hypothetical 24.1 kDa protein).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=21066552; PubMed=11145836;
Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,
Yansura D., Lewis L., Eigenbrodt C., Henzel W.J., Vandlen R.;
"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-
1Rrp."; *Cytokine* 13:1-7(2001).

RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

```
DR      EMBL; AF251119; AAG14421.1; -
DR      EMBL; BC020637; AAH20637.1; -
DR      HSSP; P18510; ILIR.
DR      InterPro; IPR000975; Interleukin_1.
DR      Pfam; PF00340; IL1; 1.
DR      ProDom; PD002536; Interleukin_1; 1.
```

DR SMART: SM00125; IL1; 1.
KW Hypothetical protein.
SO SEQUENCE 218 AA; 24138 MW; 76E09C35093DEA63 CRC64;

Query Match 88.0%; Score 895; DB 4; Length 218;

Best Local Similarity 100.08; Pred. No. 1.1e-83;
Matches 169; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 5

ID	Q9HBF2	PRELIMINARY;	PRT;	178 AA.
AC	Q9HBF2;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)			
DE	Interleukin-1-related protein short isoform.			
OS	Homo sapiens (Human).			
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21066552; PubMed=11145836;			
RA	Pan G., Risser P., Mao W., Baldwin D.T., Zhong A.W., Filvaroff E.,			
RA	Yansura D., Lewis L., Eigenbrot C., Henzel W.J., Vandlen R.;			
RT	"IL-1H, an interleukin 1-related protein that binds IL-18 receptor/IL-1			
RT	1Rrp.";			
RL	Cytokine 13:1-7(2001).			
DR	EMBL; AF251120; AAG14422.1; -.			
DR	HSSP; P18510; 1ITN.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	Pfam; PF00340; IL1; 1.			
DR	ProDom; PD002536; Interleukin_1; 1.			
DR	SMART; SM00125; IL1; 1.			
SO	SEQUENCE 178 AA; 19616 MW; D2AEACD8F8E13543 CRC64;			

Query Match	69.28;	Score 704;	DB 4;	Length 178;
Best Local Similarity	87.78;	Pred. No. 3.2e-64;		
Matches 135; Conservative	7;	Mismatches 10;	Indels 2;	Gaps 1;

[illegible]

RESULT 6

ID	Q8TD04	PRELIMINARY;	PRT;	157 AA.
AC	Q8TD04;			
DT	01-JUN-2002	(TREMBLrel. 21, Created)		
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	IL-1F7e.			
GN	IL1F7.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RT "Genomic Organization of the IL-1 Locus.";
RL Genomics 0:0-0(2002).
DR EMBL, AY071841; AAL67154.1; -.
SQ SEQUENCE 157 AA; 17459 MW; 5EA5EA10CF309086 CRC64;

Query Match	67.6%;	Score 688;	DB 4;	Length 157;
Best Local Similarity	100.0%;	Pred. No. 1.2e-62;		
Matches 130; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      63 EIFFALASSLSASAEGSPILLGVSGEFCLYCDKDKGSHPSLQLKKELMKLAOKE 122
        |||||||
Db       28 EIFFALASSLSASAEGSPILLGVSGEFCLYCDKDKGSHPSLQLKKELMKLAOKE 87
```

QY	123	SARRPFIFRQVGSWNMLESAHPHWFICTSCNCNEPVGYTDKFEENRKHIEFSFQPYCK	182
Db	88	SARRPFIFRQVGSWNMLESAHPHWFICTSCNCNEPVGYTDKFEENRKHIEFSFQPYCK	147

QY	183	AEMSPSEVSD	192
Db	148	AEMSPSEVSD	157

RESULT 7

```

ID Q9UHA5 PRELIMINARY; PRT; 157 AA.
AC Q9UHA5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Fil1 eta.
OS Homo sapiens (Human).
OC Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchem R.R., Kubin M., Garka K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
DR EMBL; AF201833; AAF25213.1; -.
DR HSSP; P10749; 2MTB.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
SQ SEQUENCE 157 AA; 17702 MW; 7A54F3D7557A3EE3 CRC64;

```

Query Match	22.5%;	Score 229;	DB 4;	Length 157;
Best Local Similarity	34.8%;	Pred. No. 1.4e-15;		
Matches 47;	Conservative 33;	Mismatches 51;	Indels 4;	Gaps 3;

QY	31	PKKFSIHDPQHVKVVLVDSGNLIAPVPDKNIYIRPEIFFALA-SLSASAEEKGSPILLGVSK	89
		::: : : :	:
Dd	9	PksyAIRDSRQMwvWLGNSNLIAAPLSRSIKPVTLHLIACRPTEFSDKEGMVYLGIKG	68
QY	90	GefCLYCDDKDGQSHPSLOLKKEKLMLAAQOKESARPFIFRAQVGSWMMLESAAHPCW	149
		: : : : : : : : : : :	:
Dd	69	KDlCfLfCAEtlGk--PTlQlKEKNIMDLVEKK-AQKPflFfhNKegStsvfQSVsYlGw	125
QY	150	FICTSCNCNEPVGYT	164
		: : :	:
Dd	126	fIATSTTGQPIELT	140

RESULT 8

ID	Q9NZH8	PRELIMINARY;	PRT;	169 AA.
AC	Q9NZH8;			
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Interleukin-1 homolog 1 (Interleukin-1 epsilon).			
GN	IL1E.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RP	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20209405; PubMed=10744718;			
RA	Kumar S., McDonnell P.C., Lehr R., Tierney L., Tzimas M.N.,			
RA	Griswold D.E., Capper E.A., Tal-Singer R., Wells G.I., Doyle M.L.,			
RA	Young P.R.;			
RT	"Identification and initial characterization of four novel members of			
RT	the interleukin-1 family.";			
RT	J. Biol. Chem. 275:10308-10314(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=AIRWAY EPITHELIAL CELLS INDUCED WITH TNF ALPHA, AND IFN;			
RA	Debets R., Timans J., Zurawski S., Bazan J.F., Kastelein R.A.;			
RT	"Novel IL-1 family member IL-1e responds through the orphan IL-1R-			
RT	related protein 2; response is antagonized by IL-1d.";			
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF200492; AAF69248.1; -			
DR	EMBL; AF206696; AAG35670.1; -			
DR	HSSP; P18510; ITTN.			
DR	InterPro; IPR000975; Interleukin_1.			
DR	Pfam; PF00340; IL1; 1.			
DR	ProDom; PD002536; Interleukin_1; 1.			
DR	SMART; SM00125; IL1; 1.			
SO	SEQUENCE 169 AA; 18721 MW; F00A9243706FA154 CRC64;			

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Query Match          22.2%; Score 225.5; DB 4; Length 169;
Best Local Similarity 38.3%; Pred. No. 3.4e-15;
Matches 51; Conservative 26; Mismatches 51; Indels 5; Gaps 4;

OY 35 SIHDQDHKVLVLDSGNLIAVPDKNYIRPEIFFALASSLSASAE-KGSPILLGVSKGEFC 93
   :|:|:|:| | | | | | :|:|:|:| | | | | | | | | | | | | | | | | |
Db 26 TINDLNQOVWTLQGQNIVAVPRSDSVTPVTAVITCKYPEALEGGRRDPYYLGIONPEMC 85

OY 94 LYCDKDKGQSHPSLQLKKKKLMKLAQKESARRPFIFYRAQVGSMMLSAHPGWFICT 153
   |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 86 LYCEKVGEQ-PTIQLKEQKINDLYGQPEPV-KPFLFYAKTGTSTLESVAFPDWFITAS 142

OY 154 SCNCNEPVGVTDK 166
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 143 S-KRDQPILITSE 154

RESULT 9
ID O9UHA7 PRELIMINARY; PRT; 158 AA.
AC O9UHA7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Trl epsilon.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20092288; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Kubin M., Garika K.E.,
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily.";
RL J. Biol. Chem. 275:1169-1175(2000).
EMBL; AF201831; AAF25211.1; -.

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[illegible]

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RESULT 10
O8R461                                PRELIMINARY;          PRT;      156 AA.
ID   Q8R461                               ID   Q8R461
AC   O8R461;                              AC   O8R461;
DT   01-JUN-2002 (TREMBLrel. 21, Created)
DT   01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE   01-JUN-2002 (TREMBLrel. 21, last annotation update)
DN   IL-1F8.
GN   IL1F8.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SWISS WEBSTER/NIH;
RA   Taylor S.L., Renshaw B.R., Garka K.E., Smith D.E., Sims J.E.;
RT   "Genomic Organization of the IL-1 Locus.";
RL   Genomics 0:0-0(2002).
DR   EMBL; AY071842; AAL67152.1; -.
SQ   SEQUENCE    156 AA;  17775 MW;  868FBEB63BF243BBF CRC64;

Query Match           19.6%; Score 199; DB 11; Length 156;
Best Local Similarity 33.3%; Pred. No. 1.6e-12;
Matches 42; Conservative 27; Mismatches 53; Indels 4; Gaps 3;

QY   30 NPKFSIHDDHKVVLVDSGNLIAVPDKNYIRPEIFFALA-SLSASAEGKSPILGVS 88
     :|::||| | || | ||| |:|: | |::|::|:
DB   7 SPRNRYRHDSQQMYWVLTGTNTLTAVPASNNVKPVLISLIACRDTEFDQVKKGGLVFLGITK 66

QY   89 KGEECLYCDKDKGSHPSLOLKKEKLMLKLAQKESARRPFIFYRAOVGSWMNLESAAHPG 148
     | |::|::|::|: | | ::|::|::|: | | ::|:
DB   67 NRNLCECCVEMEGR--PTQLKKEVDIMLYKERK-AQAFLFYHGIEGSTSVFGSVLPYG 123

QY   149 WFICTS 154
     ||| ||
DB   124 WFIATS 129

RESULT 11
Q9D6Z6                                PRELIMINARY;          PRT;      183 AA.
ID   Q9D6Z6                               ID   Q9D6Z6
AC   Q9D6Z6;                              AC   Q9D6Z6;
DT   01-JUN-2001 (TREMBlrel. 17, Created)
DT   01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE   01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DN   2310043N2ORik protein.
GN   2310043N2ORIK.
OS   Mus musculus (Mouse).
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RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cdna collection."
RL Nature 409:685-690(2001).
DR EMBL; AF230378; AAF91275.1; -
DR EMBL; AK009741; BAB26471.1; -
DR EMBL; AK008977; BAB26002.1; -
DR HSSP; P18510; 1ILR.
DR MGD; MGI:1859325; 11lf5.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; 1L1; 1.
DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; 1L1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; 1.
SQ SEQUENCE 156 AA; 17136 MW; A4D1EE2F93CF77A7 CRC64;

Query Match	18.6%;	Score 189.5;	DB 11;	Length 156;
Best Local Similarity	37.3%;	Pred. No. 1.5e-11;		
Matches	50;	Conservative	23;	Mismatches 50;
				Indels 11;
				Gaps 5;

[illegible]

QY	151	ICTSCNCNEPVGVT	164
		:	:: :
Db	122	LCTSPBADQPVRLT	135

RESULT 14
Q8R460
ID Q8R460 PRELIMINARY; PRT; 164 AA

DT	01-JUN-2002 (TREMBlrel, 21, Created)
DT	01-JUN-2002 (TREMBlrel, 21, last sequence update)
DT	01-JUN-2002 (TREMBlrel, 21, last annotation update)

05 Mus musculus (Mouse).
0C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
0C Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
0X NCBI_TaxID=10090;

RP SEQUENCE FROM N.A.
RC STRAIN-SWISS WEBSTER/NIH;
RA Taylor S.L., Renshaw B.R., Garika K.E., Smith D.E., Sims J.E.;
RT "Genomic Organization of the IL-1 Locus.";
RL Genomics 0:0-0(2002).
EMBL: AY071843: AAL67153.1; -
DR EMBL: AY071843: AAL67153.1; -
SQ SEQUENCE 164 AA; 18733 MW; A7338BD475DFEADBE CRC64;

Query Match	17.6%;	Score 178.5;	DB 11;	Length 164;
Best Local Similarity	29.9%;	Pred. No. 2.2e-10;		
Matches 49;	Conservative 29;	Mismatches 77;	Indels 9;	Gaps 5;

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QY      14 KNSFKKRLRGPVKNLNPKKFSIHQDHKVLVLDGSLIAVPDKNYIRPEIFFALASL- 72
      1 : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      4 KHPFSIHISGRE---TPDEGEVFDLDQQVMTFRNQALVTPRSRHVTPVSVTILPEKYP 59
```

QY 73 SSASAEKGPILLGVSKGEFCLYCDDKDGSHPSIQLKKREIMKLAAQKESARRPFIYR 132
| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 60 ESLEQDKGIALYLGIQNPDCKLFECKEVNG-HPTLLKEEKILDLYNHPE-PMKPETFYH 116

QY 133 A Q V G S W N M L E S A H P G W F I C T S C N C N E P Y G V T D K F E N R K H I E F S 176
: | : | | | | : | : | : | : | : | : | : |

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Db      117 TRTGCTSTESVAFPGHYIASSKTGN-PILFSKKGEYININFN 159
RESULT 15
Q9UBH0 PRELIMINARY; PRT; 155 AA.
ID      Q9UBH0

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DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FIL1 delta (Interleukin-1 like protein 1) (Interleukin-1 receptor
DE antagonist homolog 1) (Interleukin 1, delta).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
RX MEDLINE=20092888; PubMed=10625660;
RA Smith D.E., Renshaw B.R., Ketchum R.R., Rubin M., Garika K.E..
RA Sims J.E.;
RT "Four New Members Expand the IL-1 Superfamily";
RL J. Biol. Chem. 275:1169-1175(2000).

RP SEQUENCE FROM N.A.
RX MEDLINE=99443727; PubMed=10512743;
RA Mulero J.J., Pace A.M., Nelken S.T., Loeb D.B., Correa T.R.,
RA Dmanac R., Ford J.E.;
RT "IL1HY1: A Novel Interleukin-1 Receptor Antagonist Gene."; *J.*
RL Biochem. Biophys. Res. Commun. 263:702-706(1999).

RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Barton J.L., di Giovine F.S., Symons J.A., Nicklin M.J.H.;
RT "A tissue specific interleukin-1 receptor antagonist homolog from the
RT IL1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities."; [PMID:10555111](#)
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RA Barton J.L., Herbst R., Bosisio D., Nicklin M.J.H.;
RT "A tissue specific interleukin-1 receptor antagonist homolog from the
RT IL-1 cluster lacks IL-1, IL-1ra, IL-18 and IL-18ra activities."; [PMID:10530500](#)
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RX MEDLINE=20322477; PubMed=10866108;
RA Mulero J.J., Nelken S.T., Ford J.E.;
RT "Organization of the Human Interleukin-1 Receptor Antagonist Gene
IL1HY1.";
RL Immunogenetics 51:425-428(2000).

RP SEQUENCE FROM N.A.
RA Debets R., Tilmans J.C., Zurawski S., Sana T.R., Bazan F.,
RA Kastelein R.A.;
RT "Novel IL-1 ligands IL-1d and IL-1e use IL-1R related protein 2.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.

RN [7]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF126086; AAF02757.1; -
DR EMBL; AF186094; AAF02757.1; -
DR EMBL; AJ242737; CAB59822.1; -
DR EMBL; AJ242738; CAB59823.1; -
DR EMBL; AJ271338; CAB67704.1; -
DR EMBL; AF216693; AAF76981.1; -
DR EMBL; AF230377; AAF91274.1; -
DR EMBL; BC024747; AAH24747.1; -
DR HSSP; P18510; IILR.
DR InterPro; IPR000975; Interleukin_1.
DR Pfam; PF00340; IL1; 1.

DR ProDom; PD002536; Interleukin_1; 1.
DR SMART; SM00125; IL1; 1.
DR PROSITE; PS00253; INTERLEUKIN_1; UNKNOWN_1.
KW Receptor.

SQ SEQUENCE 155 AA; 16962 MW; B96DB5EFA2612E25 CRC64;

Query Match 17.0%; Score 172.5; DB 4; Length 155;
Best Local Similarity 33.6%; Pred. No. 8.4e-10;
Matches 51; Conservative 17; Mismatches 47; Indels 37; Gaps 6;

QY 34 FSIHQDQHKVLYLDSGNLIAPDPKNYIRPEIFALASSLSASAEGK----- 80
| : | | | | : | | | | : | |
Db 9 FRMKDSALKVLYLHNNQL-----LAGLHAGKVIKGEIISVVPNRWLDA 52

QY 81 --SPILGVSKGEFCLYCDKDKGQSHPSLQLKKEKIMKL-AAQKESARRPFIFYRAQVGS 137
| : : | | | | | | | | | | : | : | | | : |
Db 53 SLSPVILGVQGSQCLSC--GVGQ-EPTLTLLEPVNIMELYLGAKE--KSFTFYRRDMGL 107

QY 138 WNMLESAAHPGWFICTSCNCNEPVGVTDKFEN 169
: | | | | | | | | : | | : | | |
Db 108 TSSFESAAYPGWFLCTVPEADQPVRLTQLPEN 139

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